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NEWS	26	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS	27	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS	28	Oct 01	EVENTLINE has been reloaded
NEWS	29	Oct 04	BEILSTEIN adds new search fields
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L5 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2002 ACS  
2001:333513 Document No. 135:370654 Human and mouse **anergy**  
associated genes **GRAIL**. Ford, Gregory S.; Bloom, Debra;  
Fathman, C. Garrison (The Board of Trustees of the Leland Stanford Junior  
University, USA). ECT Int. Appl. WO 1991095943 A1 20011115, 50 pp.  
DESIGNATED STATES: W: AU, CA, JP; BW: AT, BE, CH, CY, DE, DK, ES, FI, FR,  
GB, GR, IE, IT, LU, MC, NL, PT, SE, TR. (English). CODEN: PIXXD2.  
APPLICATION: WO 2001-US15365 20010511. PRIORITY: US 2000-PV203513  
20000511.

AB Isolated nucleic acid compns. and sequences of **anergy** assocd.  
genes are provided, including the novel **GRAIL** gene. Expression  
of these genes is unregulated during the early stages of induction of  
**anergy**. The murine **GRAIL** sequence is shown to attenuate  
IL-2 transcription in T cells during response to antigenic stimulation.  
The identification of genes involved in the induction of **anergy**  
is useful in the evaluation of the pathophysiol. or immunotherapy of

cancer, autoimmune disease, and transplant rejection. Genetic sequences involved in **anergy** induction are useful markers in the evaluation of specific immunotherapies. Functional characterization of genes involved in **anergy** induction allows the elucidation of the mechanism(s) of T cell **anergy**, including the transcriptional blockade of IL-2, which may be manipulated to regulate T cell responses in human disease. The signaling pathways involving **GRAIL** are of significant interest in the identification of drugs that either block or upregulate the function(s) of **GRAIL**.

L5 ANSWER 2 OF 2 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V. DUPLICATE 1  
2001361386 EMBASE CD4(+)CD25(+) T cells facilitate the induction of T cell **anergy**. Ermann J.; Szanya V.; Ford G.S.; Paragas V.; Fathman C.G.; Lejon K.; Dr. C.G. Fathman, Stanford University Sch. of Med., Ctr. for Clinical Sci. Res. Bldg., 390 Pasteur Drive, Stanford, CA 94305-5166, United States. cfathman@stanford.edu. Journal of Immunology 167/8 (4271-4275) 15 Oct 2001.

Refs: 23.

ISSN: 0022-1767. CODEN: JOIMA3. Pub. Country: United States. Language: English. Summary Language: English.

AB T cell **anergy** is characterized by the inability of the T cell to produce IL-2 and proliferate. It is reversible by the addition of exogenous IL-2. A similar state of unresponsiveness is observed when the proliferative response of murine CD4(+)CD25(-) T cells is suppressed in vitro by coactivated CD4(+)CD25(+) T cells. We have developed a suppression system that uses beads coated with anti-CD3 and anti-CD28 Abs as surrogate APCs to study the interaction of CD4(+)CD25(+) and CD4(+)CD25(-) T cells in vitro. CD4(+)CD25(+) T cell-induced suppression, in this model, was not abrogated by blocking the B7-CTLA-4 pathway. When the CD4(+)CD25(-) T cells were separated from the CD4(+)CD25(+) suppressor cells after 24 h of coactivation by the Ab-coated beads, the CD4(+)CD25(-) T cells were unable to proliferate or to produce IL-2 upon restimulation. The induction of this anergic phenotype in the CD4(+)CD25(-) T cells correlated with the up-regulated expression of the gene related to **anergy** in lymphocytes (**GRAIL**), a novel **anergy**-related gene that acts as a negative regulator of IL-2 transcription. This system constitutes a novel mechanism of **anergy** induction in the presence of costimulation.

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L8 30 DUF REMOVE L7 (39 DUPLICATES REMOVED)

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L5 ANSWER 1 OF 30 CAPIUS COPYRIGHT 2002 ACS

2001:533513 Document No. 139:370654 Human and mouse **anergy** associated genes **GRAIL**. Ford, Gregory S.; Bloom, Debra ; Fathman, C. Garrison (The Board of Trustees of the Leland Stanford Junior University, USA). PCT Int. Appl. WO 2001085943 A1 20011115, 50 pp. DESIGNATED STATES: W: AU, CA, JP; RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR. (English). CODEN: PIXXD1. APPLICATION: WO 2001-US19385 20010511. PRIORITY: US 2000-PV203513 20000511.

AB Isolated nucleic acid compns. and sequences of **anergy** assocd. genes are provided, including the novel **GRAIL** gene. Expression of these



genes is unregulated during the early stages of induction of **anergy**. The murine GRAIL sequence is shown to attenuate IL-2 transcription in T cells during response to antigenic stimulation. The identification of genes involved in the induction of **anergy** is useful in the evaluation of the pathophysiol. or immunotherapy of cancer, autoimmune disease, and transplant rejection. Genetic sequences involved in **anergy** induction are useful markers in the evaluation of specific immunotherapies. Functional characterization of genes involved in **anergy** induction allows the elucidation of the mechanism(s) of T cell **anergy**, including the transcriptional blockade of IL-2, which may be manipulated to regulate T cell responses in human disease. The signaling pathways involving GRAIL are of significant interest in the identification of drugs that either block or upregulate the function(s) of GRAIL.

- L8 ANSWER 2 OF 30 MEDLINE DUPLICATE 1  
 2001544740 Document Number: 21475847. PubMed ID: 11591742. CD4(+)CD25(+) T cells facilitate the induction of T cell **anergy**. Ermann J; Spanya V; Ford G S; Paragas V; Fathman C G; Lejon K. (Division of Immunology and Rheumatology, Department of Medicine, Stanford University School of Medicine, Stanford, CA 94305, USA. ) JOURNAL OF IMMUNOLOGY, (2001 Oct 15) 167 (8) 4271-5. Journal code: 2985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.
- AB T cell **anergy** is characterized by the inability of the T cell to produce IL-2 and proliferate. It is reversible by the addition of exogenous IL-2. A similar state of unresponsiveness is observed when the proliferative response of murine CD4(+)CD25(-) T cells is suppressed in vitro by coactivated CD4(+)CD25(+) T cells. We have developed a suppression system that uses beads coated with anti-CD3 and anti-CD28 Abs as surrogate APCs to study the interaction of CD4(+)CD25(+) and CD4(+)CD25(-) T cells in vitro. CD4(+)CD25(+) T cell-induced suppression, in this model, was not abrogated by blocking the B7-CTLA-4 pathway. When the CD4(+)CD25(-) T cells were separated from the CD4(+)CD25(+) suppressor cells after 24 h of coactivation by the Ab-coated beads, the CD4(+)CD25(-) T cells were unable to proliferate or to produce IL-2 upon restimulation. The induction of this anergic phenotype in the CD4(+)CD25(-) T cells correlated with the up-regulated expression of the gene related to **anergy** in lymphocytes (GRAIL), a novel **anergy**-related gene that acts as a negative regulator of IL-2 transcription. This system constitutes a novel mechanism of **anergy** induction in the presence of costimulation.

- L8 ANSWER 3 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.  
 2001:41086 Document No.: PREVIEW00041086. Identification and functional characterization of a novel gene which is upregulated in anergic T cells. Ford, G. S. (1); Ermann, J. (1); Paragas, V. (1); Bloom, D. (1); Fathman, C. G. (1). (1) Stanford University School of Medicine, Palo Alto, CA USA. FASEB Journal, (April 28, 2000) Vol. 14, No. 6, pp. A1216. print. Meeting Info.: Joint Annual Meeting of the American Association of Immunologists and the Clinical Immunology Society Seattle, Washington, USA May 12-16, 2000 ISSN: 0893-6633. Language: English. Summary Language: English.

- L8 ANSWER 4 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.  
 2001:210541 Document No.: PREVIEW000210541. CD4+CD25+ cells: Facilitators of T cell **anergy**. Ermann, J. (1); Lejon, K.; Ford, G. (1); Fathman, C. G. (1). (1) Department of Medicine, Stanford University School of Medicine, Stanford, CA USA. Immunobiology, (November, 2000) Vol. 203, No. 1-2, pp. 194-195. print. Meeting Info.: Joint Annual Meeting of the German and Dutch Societies of Immunology Dusseldorf, Germany November 29-December 02, 2000 ISSN: 0171-2985. Language: English. Summary Language: English.

L8 ANSWER 5 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
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2002:106933 Document No.: PREV200200106933. **Anergy** genes.  
**Bloom, D.; Fathman, C. G.;** Slaymaker, S.. Mountain View,  
Calif. USA. ASSIGNEE: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR  
UNIVERSITY. Patent Info.: US 5747299 May 5, 1999. Official Gazette of the  
United States Patent and Trademark Office Patents, (May 5, 1999) Vol.  
1210, No. 1, pp. 451. ISSN: 0098-1133. Language: English.

L8 ANSWER 6 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)  
1998:775748 The Genuine Article (R) Number: 121HD. The induction of T  
lymphocyte **anergy**: Ras dependence and IL-2 transcription  
revisited. **Bloom D D (Reprint);** Yang Y; Moore E B; **Fathman**  
**C G.** STANFORD UNIV, SCH MED, STANFORD, CA 94305. FASEB JOURNAL (20  
MAR 1998) Vol. 12, No. 5, Part 2, Supp. [S], pp. 5378-5378. Publisher:  
FEDERATION AMER SOC EXP BIOL. 3610 ROCKVILLE PIKE, BETHESDA, MD 20814-3998  
. ISSN: 0892-6636. Pub. country: USA. Language: English.

L8 ANSWER 7 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.  
1998:103756 Document No.: PREV199800103756. The induction of T lymphocyte  
**anergy**: Ras dependence and IL-2 transcription revisited.  
**Bloom, Debra D.;** Yang, Yang; Moore, Bethany B.; **Fathman, C.**  
**Garrison.** Stanford Univ. Sch. Med., Stanford, CA 94305 USA. FASEB  
Journal, (March 20, 1998) Vol. 12, No. 5, pp. A929. Meeting Info.: Annual  
Meeting of the Professional Research Scientists on Experimental Biology  
98, Part II San Francisco, California, USA April 18-22, 1998 Federation of  
American Societies for Experimental Biology. ISSN: 0892-6638. Language:  
English.

L8 ANSWER 8 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)  
1998:1038555 The Genuine Article (R) Number: 109UX. Prolongation of cardiac  
graft survival with anti-CD4Ig plus hCTLA4Ig in primates. Krieger N R;  
Yuh D; McIntyre W B; Flavin T F; Yin D P; Robbins R; **Fathman C G**  
**(Reprint).** STANFORD UNIV, MED CTR, SCH MED, DEPT MED, DIV IMMUNOL &  
RHEUMATOL, ROOM 3-021, STANFORD, CA 94305 (Reprint); STANFORD UNIV, MED  
CTR, SCH MED, DEPT MED, DIV IMMUNOL & RHEUMATOL, STANFORD, CA 94305;  
STANFORD UNIV, MED CTR, DIV IMMUNOL, STANFORD, CA 94305. JOURNAL OF  
SURGICAL RESEARCH (MAY 1998) Vol. 76, No. 3, pp. 174-178. Publisher:  
ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS. 525 B ST, STE 1900, SAN DIEGO,  
CA 92101-4495. ISSN: 0012-4804. Pub. country: USA. Language: English.  
\*ABSTRACT IS AVAILABLE IN THE ALL JNL IALL FORMATS\*

AB Background The aim of this study was to determine whether the use of  
combined immunotherapy with a brief course of humanized anti-CD4Ig and  
hCTLA4Ig would prolong heterotopic cardiac allograft survival in primates  
(rhesus monkeys). This model was based on work in "high responder" rats  
where a brief course of depletive anti-CD4 mAb plus hCTLA4Ig was  
successful in inducing transplantation tolerance.

Methods. Heterotopic cardiac transplants were performed in rhesus  
recipients. Donor/recipient pairs between groups were confirmed to be  
reactive prior to transplantation by MLC matching. Humanized anti-CD4Ig, a  
recently developed anti-CD4 mAb, was given at a dose of 20 mg/kg i.v. on  
days -3, -2, -1, and 0. hCTLA4Ig was administered at 6 mg/kg/dose i.v. on  
days 0 and 2 for the first recipient and days 0, 2, 4, and 6 for the  
second recipient. No further immunosuppression was administered. The  
treated (n = 2) or untreated (n = 5) recipients were followed for graft  
function by daily palpitation.

Results. Treatment with anti-CD4Ig plus hCTLA4Ig resulted in a  
significant prolongation of heart graft survival (42 days for the first  
recipient and 52 days for the second recipient) compared to untreated  
recipients (7 days x 4, 11 days x 1). FACS analysis demonstrated CD4  
depletion of anti-CD4 treated animals to <2% on posttransplant day 1. The  
CD4(+) T cells gradually repopulated to 50-70% pretransplant levels just  
prior to rejection. No adverse responses (fever, tachypnea, tachycardia,

infections) were observed.

Conclusions. These are the first results demonstrating that a brief course of combined specific induction immunotherapy with humanized anti-CD4Ig plus hCTLA4Ig, in the absence of adjuvant posttransplant immunosuppression, was well tolerated and resulted in marked prolongation of cardiac allograft survival in primates. (C) 1998 Academic Press.

L8 ANSWER 9 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)

1998:363990 The Genuine Article (R) Number: 2L990. Th1 unresponsiveness can be infectious for unrelated antigens. Charlton B (Reprint); **Fathman C G**; Slattery R M. AUSTRALIAN NATL UNIV, JOHN CURTIN SCH MED RES, CANBERRA, ACT 2601, AUSTRALIA (Reprint); STANFORD UNIV, MED CTR, DEPT MED, DIV RHEUMATOL & IMMUNOL, SCH MED, STANFORD, CA 94305. IMMUNOLOGY AND CELL BIOLOGY (APR 1998) Vol. 76, No. 2, pp. 173-178. Publisher: BLACKWELL SCIENCE. 54 UNIVERSITY ST, P O BOX 378, CARLTON VICTORIA 3053, AUSTRALIA. ISSN: 0818-2641. Pub. country: AUSTRALIA; USA. Language: English.  
\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB CD4(+) T cells may be assigned a functional status (Th1 or Th2) according to the cytokines they produce including IL-2, IFN-gamma and IL-4. Th1 and Th2 CD4(+) T cells deliver different isotype-switching signals to antigen-specific B cells which bias the serum Ig isotypes. The stimulation of Th1 or Th2 responses is influenced by adjuvants and administration of antigen in IFA results in Th1 unresponsiveness as evidenced by: (i) reduced T cell proliferation to antigen; (ii) reduced IFN-gamma production in response to antigen; and (iii) reduced IgG2a isotype antigen-specific antibodies following antigen/CFA challenge. The impact of established human gamma globulin (HGG) specific Th1 unresponsiveness on subsequent immunization with an unrelated antigen, human serum albumin (HSA) in Th1-inducing CFA was then examined. When subsequently challenged with a mixture of HSA and HGG in CFA the HGG-specific Th1 unresponsiveness was infectious and dominant, preventing the induction of a Th1 response to HSA. Reduced T cell proliferation, IFN-gamma production and IgG2a antibody were consequently observed in response to HSA. The HGG-specific Th1 unresponsiveness was not infectious when HGG/CFA and HSA/CFA were administered at separate sites. This demonstrates that antigen-specific Th1 unresponsiveness can be infectious for new, molecularly unrelated antigens and supports studies showing that Th1-mediated autoimmune diseases such as experimental allergic encephalomyelitis (EAE) and diabetes can be ameliorated using antigens molecularly distinct from the disease-inducing immunogen.

L8 ANSWER 10 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)

1998:569627 The Genuine Article (R) Number: 101VR. Anti-CD4 therapy in combined heart-kidney, heart-liver, and heart small bowel allotransplants in high-responder rats. Yin D F (Reprint); Sankary H H; TalorEdwards C; Chong A S F; Foster P; Shen J K; Ma L D; Williams J W; **Fathman C G**. RUSH PRESBYTERIAN ST LUKES MED CTR, DEPT GEN SURG, SECT TRANSPLANTAT, 1653 W CONGRESS PKWY, CHICAGO, IL 60612 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, MED CTR, DIV IMMUNOL, STANFORD, CA 94305. TRANSPLANTATION (15 JUL 1998) Vol. 66, No. 1, pp. 1-9. Publisher: WILLIAMS & WILKINS. 351 WEST CAMDEN ST, BALTIMORE, MD 21201-2436. ISSN: 0041-1337. Pub. country: USA. Language: English.  
\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Background. In these experiments, we studied the role of anti-CD4 (Ox33) monoclonal antibody in the induction of allograft unresponsiveness in high-responder Lewis rats in the single liver, kidney, small bowel, and heart versus the combined heart-kidney, heart-liver, and heart-small bowel transplantation models.

Methods. ACI heart, kidney, liver, and small bowel allografts were transplanted into untreated and anti-CD4 treated Lewis rats. In selected animals bearing long-surviving ACI liver or kidney allografts for over 3 months, donor-matched second heart or third-party (Brown Norway) heart allografts were transplanted. Simultaneously, heart-liver, heart-kidney,

and heart-small bowel transplants were performed on the day of operation. Rejected allografts were verified by autopsy and pathology.

Results. ACI liver allografts were permanently accepted by Lewis recipients treated with either regular-dose (5 mg/kg for 4 days) or low-dose (5 mg/kg for 2 days) of anti-CD4 monoclonal antibody. Pretransplant anti-CD4 therapy (5 mg/kg for 4 days but not 5 mg/kg for 2 days) resulted in a long-term survival of kidney allografts (mean survival time [MST] >100.0 days, n=5). Pretransplant anti-CD4 treatment (5 mg/kg for 4 days) could not induce tolerance when single ACI hearts were transplanted; however, long-term survival of ACI heart allografts could be induced when heart transplants were combined with liver (n=7) or kidney (n=8) transplants. The survival of both ACI heart allografts (MST=25.0 days, n=4) and small bowel allografts (MST=28.0 days, n=4) was also prolonged when simultaneous heart and small bowel transplantation was performed in anti-CD4-treated recipients. The second ACI heart allograft was permanently accepted by tolerant Lewis recipients of ACI liver or kidney allografts induced by anti-CD4 treatment, and third-party heart grafts were acutely rejected without affecting survival of the primary allografts.

Conclusion. Our current results show that: (1) there is a vigorous rejection of heart greater than or equal to small bowel + kidney + liver in high-responder Lewis rats after pretransplant anti-CD4 therapy; and (2) simultaneous or metachronous combined liver-heart and kidney-heart transplants may protect heart allografts from rejection.

L8 ANSWER 11 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)  
97:162574 The Genuine Article (R) Number: WH142. Understanding the mechanism of T lymphocyte **anergy**. Bloom D (Reprint); Moore B; Fathman C G. STANFORD UNIV, STANFORD, CA 94305. JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY (JAN 1997) Vol. 99, No. 1, Part 2, Supp. [S], pp. 1256-1256. Publisher: MOSBY-YEAR BOOK INC. 11830 WESTLINE INDUSTRIAL DR, ST LOUIS, MO 63146-3318. ISSN: 0091-6749. Pub. country: USA. Language: English.

L8 ANSWER 12 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.  
1997:144773 Document No.: PREV199799443976. Understanding the mechanism of T lymphocyte **anergy**. Bloom, Debra; Moore, Bethany; Fathman, C. G.. Stanford Univ., Stanford, CA USA. Journal of Allergy and Clinical Immunology, (1997) Vol. 99, No. 1 PART 2, pp. S307. Meeting Info.: Joint Meeting of the American Academy of Allergy, Asthma and Immunology, the American Association of Immunologists and the Clinical Immunology Society San Francisco, California, USA February 21-26, 1997 ISSN: 0091-6749. Language: English.

L8 ANSWER 13 OF 30 CASLUS COPYRIGHT 2002 ACS  
1996:134201 Document No. 124:173452 Human gene and gene product associated with **anergy** and their diagnostic uses. Bloom, Debra; Fathman, Garrison (Board of Trustees of the Leland Stanford Junior University, USA). PCT Int. Appl. WO 9600300 A1 19960104, 30 pp. DESIGNATED STATES: W: CA, JP; RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). COLEN: PIXXD2. APPLICATION: WO 1995-US7958 19950622. PRIORITY: US 1994-265100 19940623.

AB Genes assocd. with the induction of **anergy** in T-cells and methods of detecting them and the use of the genes or proteins as diagnostics for monitoring induction of tolerance for the presence of tolerized T-cells in a physiol. sample, or elucidating the pathway to **anergy** or activation in T-cells are described. A cysteine string protein is found to indicate quiescent T-cells and is lost with anergic T-cells. cDNAs assocd. with **anergy** were cloned from an anergic T-cell clone by differential display.

L8 ANSWER 14 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)  
96:277058 The Genuine Article (R) Number: UE192. QUANTITATIVE-ANALYSIS OF

T-CELL ACTIVATION - ROLE OF TCR LIGAND DENSITY AND TCR AFFINITY. KIM D T; ROTHBARD J B; **BLOOM D D; FATHMAN C G (Reprint)**. STANFORD UNIV, SCH MED, DEPT MED, DIV RHEUMATOL & IMMUNOL, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, DIV RHEUMATOL & IMMUNOL, STANFORD, CA, 94305. JOURNAL OF IMMUNOLOGY (15 APR 1996) Vol. 156, No. 8, pp. 2737-2742. ISSN: 0022-1767. Pub. country: USA. Language: ENGLISH.

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB (B6A)F-1 mice were immunized with sperm whale myoglobin, and T cell clones and hybridomas were generated. Hybridoma 74a.e9 was specific for the sperm whale myoglobin 67-79 peptide and could be partially activated by a peptide analogue, equine myoglobin with a natural 74G substitution. Using this hybridoma in T cell activation assays, we studied the effects of varying the avidity of the TCR for its ligand, the concentration of MHC:peptide complex in the APC, and the density of TCR on the surface. Varying ligand concentration on the surface of the APC, the TCR avidity, or the density of TCR on the T cell were equally important parameters in driving T cell activation. The mouse myoglobin (74T) analogue, however, acted as an antagonist to the T cell response. Its effectiveness was also partially determined by its ability to bind to MHC. By independently altering each of these variables and following T cell activation, we describe the interrelationships among these three components (MHC:peptide:TCR) that control the activation of the T cell.

L8 ANSWER 15 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)  
95:404780 The Genuine Article (R) Number: R0619. CD4-POSITIVE SUPPRESSOR CELLS BLOCK ALLOTRANSPLANT REJECTION. YIN D P; **FATHMAN C G (Reprint)**. STANFORD UNIV, SCH MED, DIV IMMUNOL & RHEUMATOL, ROOM 3041, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, STANFORD, CA, 94305; STANFORD UNIV, SCH MED, DEPT SURG, STANFORD, CA, 94305. JOURNAL OF IMMUNOLOGY (15 JUN 1995) Vol. 154, No. 12, pp. 6339-6345. ISSN: 0022-1767. Pub. country: USA. Language: ENGLISH.

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Mechanisms of maintenance of transplantation tolerance induced in adult rats by depletive regimens of anti-CD4 before transplantation of vascularized heart allografts were studied. Despite the fact that there has been little evidence that tolerant lymphocytes could prevent allograft rejection after adoptive transfer, we demonstrated a suppressive role for lymphocytes from tolerant animals in vivo. These experiments analyzed the ability of lymphocytes from tolerant rats to protect passenger leukocyte-depleted Lewis heart grafts that had been "parked" in ACI rats (treated with pretransplant anti-CD4 and maintained for >100 days) compared with their ability to protect transplantation of fresh Lewis heart grafts in naive ACI rats. Although parked Lewis heart grafts were rejected in unmanipulated ACI recipients, parked hearts (but not naive Lewis heart allografts), were permanently accepted by naive ACI rats when syngeneic tolerant spleen cells were adoptively transferred at the time of transplantation. Further, we demonstrated that the suppressor cells in the tolerant spleen cells were CD4(+). These results suggest that CD4(+) spleen cells from tolerant rats inhibit allograft recognition and may maintain allograft tolerance by blocking the indirect pathway of allorecognition.

L8 ANSWER 16 OF 30 SCISEARCH COPYRIGHT 2002 ISI (R)  
95:535015 The Genuine Article (R) Number: R0464. INDUCTION OF TOLERANCE TO HEART ALLOGRAFTS IN HIGH RESPONDER RATS BY COMBINING ANTI-CD4 WITH CTLA4IG . YIN D P; **FATHMAN C G (Reprint)**. STANFORD UNIV, SCH MED, DEPT MED, DIV IMMUNOL & RHEUMATOL, ROOM 3-021, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, SCH MED, DEPT MED, DIV IMMUNOL & RHEUMATOL, STANFORD, CA, 94305. JOURNAL OF IMMUNOLOGY (15 AUG 1995) Vol. 155, No. 4, pp. 1655-1659. ISSN: 0022-1767. Pub. country: USA. Language: ENGLISH.

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB It has been difficult to induce donor-specific transplantation

tolerance in high responder Lewis rats, Results presented below demonstrate that amounts of pretransplant anti-CD4 sufficient to allow allograft tolerance in low responder strains (5 mg/kg x 4 days) did not prevent the acute rejection of ACI heart allografts in high responder Lewis recipients. Higher doses of pretransplant anti-CD4 (10 mg/kg, 15 mg/kg, and 20 mg/kg) given alone could delay but not prevent allograft rejection. Pretransplant anti-CD4 combined with anti-CD8, thymectomy, and total lymphoid irradiation all failed to produce tolerance to ACI heart allografts. However, a regimen of anti-CD4 combined with CTLA4Ig allowed indefinite survival of ACI heart allografts (mean survival time, >100 day). Second-donor matched heart grafts were permanently accepted, and third-party heart allografts were rejected by the tolerant recipients. These results suggest a new combination therapeutic strategy for clinical transplantation.

L8 ANSWER 17 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.  
 1994:298453 Document No.: PREV199497298453. Mechanisms of transplantation tolerance. Charlton, Brett (1; Auchincloss, Hugh, Jr.; **Fathman, C. Garrison (1)**). (1) Stanford Univ. Sch. Med., Dep. Med., Div. Immunol. and Rheumatol., Stanford, CA 94305 USA. Paul, William E. [Editor]. Annual Review of Immunology, (1994) Vol. 12, pp. 707-734. Annual Review of Immunology. Publisher: Annual Reviews Inc. P.O. Box 10139, 4139 El Camino Way, Palo Alto, California 94306, USA. ISSN: 0732-0582. ISBN: 0-8243-3012-9. Language: English.

L8 ANSWER 18 OF 30 MEDLINE DUPLICATE 3  
 95226015 Document Number: 95226015. PubMed ID: 7710719. Regulation of autoimmune response. Ridgway W M; Weiner H L; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, California 94305. ) CURRENT OPINION IN IMMUNOLOGY, (1994 Dec) 6 (6) 946-95. Ref: 51. Journal code: 8900118. ISSN: 0952-7915. Pub. country: ENGLAND: United Kingdom. Language: English.

AB Recent work on such apparently disparate fields as T-cell receptor peptide-induced regulation, superantigens, antigen-induced tolerance, models of peripheral tolerance, apoptosis, and T-cell receptor antagonists demonstrates a similarity in immune response from a regulatory perspective. In many systems, a 'tolerance' pathway is observed, characterized broadly as an initial disturbance in the immune system, with a resulting predominance of effector cells, followed by a homeostatic response (often requiring CD8+ cells) which leads the effector population into T-cell receptor downregulation, T-cell inactivation, **anergy** and, often, eventual apoptotic death. In the regulated immune response, mixed populations of anergized and apoptosing T cells can be found. In some cases, **anergy** appears to lead to death while, in other instances, cells revert to a functional state. This review focuses on recent papers examining each of these topics in an attempt to obtain a preliminary integrated picture of immune regulation in autoimmune diseases.

L8 ANSWER 19 OF 30 MEDLINE DUPLICATE 4  
 94280734 Document Number: 94280734. PubMed ID: 8011295. Mechanisms of transplantation tolerance. Charlton B; Auchincloss H Jr; **Fathman C G**. (Stanford University School of Medicine, Department of Medicine, California 94305. ) ANNUAL REVIEW OF IMMUNOLOGY, (1994) 12 707-34. Ref: 216. Journal code: 8309204. ISSN: 0732-0582. Pub. country: United States. Language: English.

AB Transplantation tolerance, the long-term acceptance of grafted tissue in the absence of continuous immunosuppression, remains an elusive goal in humans, but it has been achieved in animal models using numerous approaches. The mechanisms behind graft acceptance vary according to the means used to create the state of acceptance. Several major mechanisms can now be recognized. While thymic deletion of T cells appears to be a mainstay of self-tolerance, its role in transplantation tolerance now

seems to be less significant. In contrast, extrathymic mechanisms of transplantation tolerance seem to be major factors in long-term graft acceptance. If donor antigens are presented in a nonimmunogenic manner on the graft, e.g. due to modification of graft tissue by culture, peripheral T cells of the recipient may ignore the graft. Alternatively, nonstimulatory presentation of donor antigens on graft tissue can induce a state of unresponsiveness in recipient T cells, i.e. **anergy**, rather than activating them to destroy the graft. Suppression mechanisms also operate to control graft rejection and may be specific or nonspecific in nature. Specific suppression mechanisms might act in an idiosyncratic or antigen-specific fashion, and evidence is accumulating that this may be mediated through the elaboration of cytokines. Donor antigen-specific T cells may be activated to produce "protective" cytokines which then regulate the generation of destructive T cells. Future therapies will be aimed at affecting graft acceptance through these peripheral mechanisms.

L8 ANSWER 20 OF 30 MEDLINE DUPLICATE 5  
 95142881 Document Number: 95142881. PubMed ID: 7840850. Prevention of diabetes and insulinitis by neonatal intrathymic islet administration in NOD mice. Charlton B; Taylor-Edwards C; Tisch R; **Fathman C G**. (Department of Medicine, Stanford University Medical School CA 94305. ) JOURNAL OF AUTOIMMUNITY, (1994 Oct) 7 (5) 549-60. Journal code: 8812164. ISSN: 0896-8411. Pub. country: ENGLAND: United Kingdom. Language: English.

AB The murine model of human insulin dependent diabetes mellitus (IDDM), the non-obese diabetic (NOD) mouse, develops a T cell-dependent destruction of pancreatic islets. While the target antigens are unknown, there is clearly a lack of tolerance to them. Neonatal intrathymic (i.t.) antigen injection has been successfully employed to prevent insulinitis in BB rats but previous i.t. islet antigen studies in NOD mice were done on older mice. We have injected syngeneic islets into the thymus of NOD mice at birth and found that diabetes and insulinitis can be completely prevented by this procedure. The effect is islet antigen-specific since other T cell responses, including autoimmune salivary infiltration, are unaffected. Furthermore, contrary to previous studies, cyclophosphamide administration was unable to induce diabetes in treated mice which suggests that deletion or **anergy** might be the mechanism by which neonatal intrathymic islet injection protects from disease. However, anti-islet antigen antibodies were still present in these mice which suggests that the mechanism of disease protection may be more complex.

L8 ANSWER 21 OF 30 MEDLINE DUPLICATE 6  
 93203626 Document Number: 93203626. PubMed ID: 7681087. SEB induced **anergy**: modulation of immune response to T cell determinants of myoglobin and myelin basic protein. Gaur A; **Fathman C G**; Steinman L; Brocke S. (Department of Medicine, Stanford University School of Medicine, CA 94305. ) JOURNAL OF IMMUNOLOGY, (1993 Apr 1) 150 (7) 3062-9. Journal code: 2985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.

AB Superantigens have the ability to stimulate a subset of T cells based upon their expressed TCR beta-chain. It has been demonstrated that the administration of staphylococcal enterotoxin B (SEB) in mice leads to unresponsiveness in V beta 8+ T cells in vivo which are the same T cells that could be stimulated in vitro by this enterotoxin. We present here data on the effect of SEB administration in DBA/2 and (PL/J x SJL)F1 mice on their T cell response to two different T cell determinants, the responses against which are dominated by the use of V beta 8+ T cells. Treatment of mice with SEB not only diminished their primary T cell proliferative response to these determinants, but also was able to effectively reduce the memory T cell response. SEB treatment, however, showed only a modest effect in preventing Ac 1-11-induced experimental autoimmune encephalomyelitis in H-2u mice.

L8 ANSWER 22 OF 30 SCISEARCH COPYRIGHT 2001 ISI (F)

93:617120 The Genuine Article (R) Number: MB846. INDUCTION OF RELAPSING PARALYSIS IN EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS BY BACTERIAL SUPERANTIGEN. BROCKE S (Reprint); GAUR A; PIERCY C; GAUTAM A; GIJBELS K; **FATHMAN C G**; STEINMAN L. STANFORD UNIV, MED CTR, SCH MED, DEPT NEUROL & NEUROL SCI, STANFORD, CA, 94305 (Reprint); STANFORD UNIV, MED CTR, SCH MED, DEPT MED, STANFORD, CA, 94305. NATURE (14 OCT 1993) Vol. 365, No. 6447, pp. 642-644. ISSN: 0028-0836. Pub. country: USA. Language: ENGLISH.

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB THE role of infection in the pathogenesis of clinical relapses that occur in most autoimmune diseases, including multiple sclerosis, remains to be established<sup>1,2</sup>. Experimental autoimmune encephalomyelitis (EAE) serves as a model for multiple sclerosis, with episodes of relapsing paralysis<sup>3-9</sup>. In certain strains of mice, T-lymphocytes expressing the Vbeta8 T-cell receptor (TCR)6-8 engage the amino-terminal epitope Acl-11 of myelin basic protein, leading to EAE. The bacterial superantigen staphylococcal enterotoxin B (SEB) activates Vbeta8-expressing T cells. Here we show that after immunization with Acl-11, or after transfer of encephalitogenic T-cell lines or clones reactive to Acl-11, SEB induces exacerbation or relapses of paralytic disease in mice that are in clinical remission following an initial episode of paralysis, and triggers paralysis in mice with subclinical disease. Tumour necrosis factor has a critical role in the mechanism underlying SEB-induced exacerbation of disease, because anti-tumour necrosis factor antibody given in vivo delays the onset of paralysis triggered by SEB. On reactivation of autoaggressive cells through their T-cell receptor, superantigens may induce clinical relapses of autoimmune disease.

L8 ANSWER 23 OF 30 MEDLINE DUPLICATE 7  
94025871 Document Number: 94025071. PubMed ID: 8212181. Evidence that clonal **anergy** is induced in thymic migrant cells after anti-CD4-mediated transplantation tolerance. Alters S E; Song H K; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, California 94305-5111. : TRANSPLANTATION, (1993 Sep) 56 (3) 633-8. Journal code: 0132144. ISSN: 0041-1337. Pub. country: United States. Language: English.

AB Diabetic (B6) (IE-) mice treated with a depleting regimen of anti-CD4 monoclonal antibody at the time of transplantation with A/J (IEK) islets of Langerhans showed indefinite acceptance of their islet allograft, as evidenced by persistent normoglycemia. To address the mechanisms involved in such anti-CD4 induced transplantation tolerance we studied potentially IE-reactive V beta 11+ T cells from the tolerant allografted mice. Following complete repopulation of the CD4+ cells, both the CD4+V beta 11+ and CD8+V beta 11+ T cell subsets of the transplanted mice were unresponsive to anti-V beta 11 specific crosslinking. In contrast, lymphocytes tested within the first ten days following transplant were responsive to anti-V beta 11 specific crosslinking; this response decreased as a function of time and reached background levels by day 120 posttransplant. Sorting experiments indicated that the response of lymphocytes to anti-V beta 11 specific crosslinking seen during the initial 120 days posttransplant was confined to the peripheral CD8+ cells; the repopulating CD4+V beta 11+ T cells were unresponsive. In addition, administration of r-IL-2 at the time of transplantation induced rejection in anti-CD4-treated animals, again indicating that the peripheral CD8+ cells could respond shortly after transplant if provided with appropriate help. The decreasing response of CD8+ T cells from transplanted animals to anti-V beta 11 stimulation was inversely correlated with the rate of migration of cells from the thymus to the periphery, implying that new thymic migrant V beta 11+ cells, both CD4+ and CD8+, were rendered anergic upon encountering peripheral alloantigen. These data suggest the possibility that recent thymic migrants are rendered anergic upon encountering antigen in the periphery, a simple model to serve as a "fail-safe" mechanism to prevent autoreactivity.



- L8 ANSWER 24 OF 30 MEDLINE DUPLICATE 8  
 93127211 Document Number: 93127221. PubMed ID: 8420037. Evidence that anti-CD8 abrogates anti-CD4-mediated clonal **anergy** but allows allograft survival in mice. Song H K; Alters S E; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, California 94305-5111. ) TRANSPLANTATION, (1993 Jan) 55 (1) 133-9. Journal code: 0132144. ISSN: 0041-1337. Pub. country: United States. Language: English.
- AB Monoclonal antibodies directed against different T cell subpopulations have been used in several rodent models of transplantation to induce long-term unresponsiveness to allografts by a variety of mechanisms. To investigate whether different mechanisms may be operative when different regimens of mAb therapy are used, we studied the effects of various combinations of anti-T-cell antibody treatment on the induction of tolerance in a mouse islet allograft model. Anti-CD4 mAb alone, anti-CD8 mAb alone, anti-CD4 mAb plus anti-CD8 mAb, and anti-Thy1.2 mAb alone were given at the time of engraftment. Only the anti-CD4 mAb and the anti-CD4 mAb plus anti-CD8 mAb regimens were successful in inducing permanent unresponsiveness to islet allografts. We have previously shown that anti-CD4 mAb alone induces permanent unresponsiveness to islet allografts by a mechanism of clonal **anergy**, as demonstrated by unresponsiveness of potentially alloreactive T cells to anti-T-cell receptor-specific cross-linking. Interestingly, the potentially alloreactive T cell subsets of recipient mice (V beta 5+ and V beta 11+) made unresponsive to islet allografts by anti-CD4 mAb plus anti-CD8 mAb therapy were not found to be anergic using the same assay. Differences between the repopulation kinetics of CD8+ T cells of anti-CD4 mAb plus anti-CD8 mAb treated recipient mice, which accepted islet allografts, and anti-Thy1.2 treated recipient mice, which rejected islet allografts despite similar levels of initial T cell depletion, suggest that unresponsiveness to alloantigen may have been induced in anti-CD4 mAb plus anti-CD8 mAb treated recipients by clearance of donor passenger leukocytes during prolonged CD8+ T cell depletion.
- L8 ANSWER 25 OF 30 MEDLINE DUPLICATE 9  
 93117858 Document Number: 93117858. PubMed ID: 8418801. Requirement for CD8+ cells in T cell receptor peptide-induced clonal unresponsiveness. Gaur A; Ruberti G; Haspel R; Mayer J F; **Fathman C G**. (Department of Medicine, Stanford University School of Medicine, CA 94305. ) SCIENCE, (1993 Jan 1) 259 (5091) 91-4. Journal code: 0404511. ISSN: 0036-8075. Pub. country: United States. Language: English.
- AB T cell receptor (TCR) vaccination in rats prevents the development of experimental allergic encephalomyelitis (EAE), an animal model of multiple sclerosis. The mechanism of this potential immunotherapy was examined by vaccinating mice with an immunogenic peptide fragment of the variable region of the TCR V beta 8.2 gene. Another immunogen that usually induces an immune response mediated by V beta 8.2+ T cells was subsequently inhibited because specific clonal unresponsiveness (**anergy**) had been induced. Depletion of CD8+ cells before TCR peptide vaccination blocked such inhibition. Thus, the clonal **anergy** was dependent on CD8+ T cells, and such immunoregulatory T cells may participate in the normal course of EAE.
- L8 ANSWER 26 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 10  
 1993:141685 Document No.: PREV199344114885. **Anergy** induced by synthetic peptides of myelin basic protein blocks progression of autoimmune encephalomyelitis. Gaur, Amitabh (1); Waters, B. (1); Rothbard, J.; **Fathman, C. Garrison**. (1) Div. Immunol. Rheumatol., Dep. Med., Stanford Univ. Med. Cent., Stanford, CA 94305 USA. Journal of Cellular Biochemistry Supplement, (1993) Vol. 0, No. 17 PART C, pp. 68. Meeting Info.: Keystone Symposium on Emerging Principles for Vaccine

Development: Antigen Processing and Presentations Taos, New Mexico, USA  
February 8-14, 1993 ISSN: 0732-1959. Language: English.

L8 ANSWER 27 OF 30 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 11

1992:192861 Document No.: BR43:5211. CLONAL **ANERGY** INDUCED IN THYMIC MIGRANT CELLS DURING ANTI-CD4 INDUCED TRANSPLANTATION TOLERANCE. ALTERS S E; SONG H K; **FATHMAN C G**. DEP. MED./IMMUNOL., S-021, STANFORD UNIV. SCH. MED., STANFORD, CALIF. 94305.. MEETING OF THE FEDERATION OF AMERICAN SOCIETIES FOR EXPERIMENTAL BIOLOGY (FASEB) PART II, ANAHEIM, CALIFORNIA, USA, APRIL 5-9, 1992. FASEB (FED AM SOC EXP BIOL) J. (1992) 6 (5), A1702. CODEN: FAJOEC. ISSN: 0892-8638. Language: English.

L8 ANSWER 28 OF 30 MEDLINE DUPLICATE 12  
93068334 Document Number: 93068334. PubMed ID: 1279312. Amelioration of autoimmune encephalomyelitis by myelin basic protein synthetic peptide-induced **anergy**. Gaur A; Wiers B; Liu A; Rothbard J; **Fathman C G**. (Stanford University School of Medicine, Division of Immunology and Rheumatology, CA 94305. ) SCIENCE, (1992 Nov 27) 258 (5087) 1491-4. Journal code: 0404511. ISSN: 0036-8075. Pub. country: United States. Language: English.

AB Experimental autoimmune encephalomyelitis (EAE), a demyelinating disease of the central nervous system that can be induced in susceptible strains of mice by immunization with myelin basic protein (MBP) or its immunodominant T cell determinants, serves as a model of human multiple sclerosis. Tolerance to MBP in adult mice was induced by intraperitoneal injection of synthetic peptides of immunodominant determinants of MBP and prevented MBP-induced EAE. Furthermore, tolerance-inducing regimens of peptides administered to mice after the disease had begun (10 days after induction with MBP) blocked the progression and decreased the severity of EAE. Peptide-induced tolerance resulted from the induction of **anergy** in proliferative, antigen-specific T cells.

L8 ANSWER 29 OF 30 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.DUPLICATE 13  
92355607 EMBASE Document No.: 1992355607. Anti-CD4 monoclonal antibodies in therapy: Creation of nonclassical tolerance in the adult. Shizuru J.A.; Alters S.E.; **Fathman C.G.**. Stanford Univ. School of Medicine, Div. of Rheumatology and Immunology, Stanford, CA 94305, United States. Immunological Reviews -/129 (105-130) 1992. ISSN: 0105-2896. CODEN: IMPEDL. Pub. Country: Denmark. Language: English. Summary Language: English.

AB We have described the studies from our laboratory which demonstrate that depleting anti-CD4 mAb induce tolerance to foreign antigens in adult, euthymic animals. Further, we have proposed that such tolerance occurs as a result of new thymic migrants encountering antigens in the periphery. However, these conclusions can be considered only partial since we (Song et al. in press) and others have shown that depletion of T cells per se does not permit tolerance. For example, anti-Thy-1 or anti-Lyt-1 are themselves immunosuppressive and able to deplete T cells, yet they elicit strong anti-gluculin responses against themselves and do not permit tolerance to be induced either to transplants or administered soluble protein antigen. We have recently found that while the combination of anti-CD4 and anti-CD8 mAb allows long-term survival of allografted islets in mice, **anergy** in the relevant T-cell subsets was not found (in contrast to what is found with anti-CD4 mAb treatment alone) (Song et al. in press). In this instance, long-term survival was probably the result of changes in graft immunogeneity (i.e., migration of passenger leukocytes) since the kinetics of repopulation were much delayed in the anti-CD4 and -CD8 treated mice. As discussed elsewhere in this volume, interesting studies from several laboratories suggest that non-depleting anti-CD4 mAb can generate unresponsiveness in a variety of systems. In reviewing the literature it is clear that the success of non-depleting reagents appears to be dependent upon the model system tested. For example, although

depleting and nondepleting CD4 mAb regimens produced comparable prolongation of cultured fetal pancreas allografts in mice (Charlton and Mandel), almost total elimination of circulating CD4+ cells did not prevent acute rejection of murine skin grafts (Auchincloss et al. 1988). This heterogeneity is not surprising given the multiple functional roles of the CD4 molecule and the cells that bear this molecule. In addition to depletion, antibodies directed against CD4 can potentially affect CD4+ cell function by (1) direct blockade or failure to augment the formation of the TCR-antigen/MHC ternary complex or (2) by transmitting a negative signal to the CD4 T cell or interfering with normal signal transduction mechanisms. Undoubtedly, it is a combination of mechanisms that allows these antibodies their immunosuppressive effects. What can be said with certainty is that these antibodies will continue to be important tools for understanding the molecular and cellular basis of the immune response, and will soon emerge as invaluable therapeutic agents in the clinical arena.

L8 ANSWER 10 OF 30 MEDLINE DUPLICATE 14  
 91108348 Document Number: 91108348. PubMed ID: 1899105. Anti-CD4 mediates clonal **anergy** during transplantation tolerance induction. Alters S E; Shizuru J A; Ackerman C; Grossman D; Seydel K B; Fathman C G . (Department of Medicine, Stanford University School of Medicine, California 94305. ) JOURNAL OF EXPERIMENTAL MEDICINE, (1991 Feb 1) 173 (2) 491-4. Journal code: 2985109R. ISSN: 0022-1007. Pub. country: United States. Language: English.

AB Depletion of CD4+ cells using anti-CD4 monoclonal antibodies leads to allograft tolerance. Here we show that anti-CD4-mediated tolerance to pancreatic islets of Langerhans transplanted from an A/J (IEK) donor to a diabetic C57Bl/6 (B6) (IE-) recipient occurs in the absence of clonal deletion of the potentially IE-reactive V beta 11+ T cells. Instead, a state of clonal **anergy** is induced in both the CD4+V beta 11+ and CD8+V beta 11+ T cell subsets. This clonal **anergy** can be partially overcome in vitro by the addition of recombinant interleukin 2.

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FILE 'MEDLINE, EMBASE, BIOSIS, SCISEARCH, CAPLUS' ENTERED AT 08:24:54 ON 31 OCT 2002

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 L2 1987 S GRAIL  
 L3 181 S L3 AND PROTEIN  
 L4 3 S L3 AND ANERGY  
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 L7 29 S L6 AND ANERGY  
 L8 30 DUP REMOVE L7 (39 DUPLICATES REMOVED)

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L10 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2002 ACS

2001:933513 Document No. 135:370654 Human and mouse **anergy**

associated genes **GRAIL**. Ford, Gregory S.; Bloom,

Debra; Fathman, C. Garrison (The Board of Trustees of the

Leland Stanford Junior University, USA). PPT Int. Appl. WO 2001085943 A1

20011115, 50 pp. DESIGNATED STATES: W: AU, CA, JP; PW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR. (English). CODEN: PIMXD2. APPLICATION: WC 2001-US15385 20010511. PRIORITY: US 2000-PV-03513 20000511.

AB Isolated nucleic acid compns. and sequences of **anergy** associ. genes are provided, including the novel **GRAIL** gene. Expression of these genes is unregulated during the early stages of induction of **anergy**. The murine **GRAIL** sequence is shown to attenuate IL-2 transcription in T cells during response to antigenic stimulation. The identification of genes involved in the induction of **anergy** is useful in the evaluation of the pathophysiol. or immunotherapy of cancer, autoimmune disease, and transplant rejection. Genetic sequences involved in **anergy** induction are useful markers in the evaluation of specific immunotherapies. Functional characterization of genes involved in **anergy** induction allows the elucidation of the mechanism(s) of T cell **anergy**, including the transcriptional blockade of IL-2, which may be manipulated to regulate T cell responses in human disease. The signaling pathways involving **GRAIL** are of significant interest in the identification of drugs that either block or upregulate the function(s) of **GRAIL**.

L10 ANSWER 2 OF 2 MEDLINE

2001544740 Document Number: 21475847. PubMed ID: 11591749. CD4(+)CD25(+) T cells facilitate the induction of T cell **anergy**. Ermann J; Szanya V; Ford G S; Paragas V; Fathman C G; Lejon K. (Division of Immunology and Rheumatology, Department of Medicine, Stanford University School of Medicine, Stanford, CA 94305, USA. ) JOURNAL OF IMMUNOLOGY, (2001 Oct 15) 167 (8) 4271-5. Journal code: 1985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.

AB T cell **anergy** is characterized by the inability of the T cell to produce IL-2 and proliferate. It is reversible by the addition of exogenous IL-2. A similar state of unresponsiveness is observed when the proliferative response of murine CD4(+)CD25(-) T cells is suppressed in vitro by coactivated CD4(+)CD25(+) T cells. We have developed a suppression system that uses beads coated with anti-CD3 and anti-CD28 Abs as surrogate APCs to study the interaction of CD4(+)CD25(+) and CD4(+)CD25(-) T cells in vitro. CD4(+)CD25(+) T cell-induced suppression, in this model, was not abrogated by blocking the B7-CTLA-4 pathway. When the CD4(+)CD25(-) T cells were separated from the CD4(+)CD25(+) suppressor cells after 24 h of coactivation by the Ab-coated beads, the CD4(+)CD25(-) T cells were unable to proliferate or to produce IL-2 upon restimulation. The induction of this anergic phenotype in the CD4(+)CD25(-) T cells correlated with the up-regulated expression of the gene related to **anergy** in lymphocytes (**GRAIL**), a novel **anergy**-related gene that acts as a negative regulator of IL-2 transcription. This system constitutes a novel mechanism of **anergy** induction in the presence of costimulation.

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COST IN U.S. DOLLARS

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FULL ESTIMATED COST	89.53	89.74
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	ENTRY	SESSION
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Perfect score: 1774

Sequence: 1 actgagactccacgcggt.....ataggcaagttctctctcag 1774

Scoring table: IDENTITY\_NUC

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109290

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: em\_mu.\*
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- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
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- 33: em\_hgt\_mus.\*
- 34: em\_hgt\_pln.\*
- 35: em\_hgt\_rod.\*
- 36: em\_hgt\_vrt.\*
- 37: em\_hgt\_mam.\*
- 38: em\_sy.\*
- 39: em\_hgt\_hum.\*
- 40: em\_hgt\_mus.\*
- 41: em\_hgtg\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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3	1280.8	72.2	1297	9	AF394689 Homo sapi
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8	674.4	38.0	169812	9	AL391315 Human DNA
9	674.4	38.0	169863	2	AL591467 Homo sapi
10	392.2	22.1	404	6	AK071980 Sequence
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12	330.0	17.5	435	6	AX396961 Sequence
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14	278.4	15.7	167021	2	AC111461 Rattus no
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## ALIGNMENTS

RESULT 1	AX337968	Sequence	9	from Patent	2796 bp	DNA	linear	PAT 09-JAN-2002
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ACCESSION	AX337968	Sequence	9	from Patent	2796 bp	DNA	linear	PAT 09-JAN-2002
VERSION	AX337968.1	Sequence	9	from Patent	2796 bp	DNA	linear	PAT 09-JAN-2002
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SOURCE	AX337968.1	Sequence	9	from Patent	2796 bp	DNA	linear	PAT 09-JAN-2002
ORGANISM	AX337968.1	Sequence	9	from Patent	2796 bp	DNA	linear	PAT 09-JAN-2002
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AUTHORS	AX337968.1	Sequence	9	from Patent	2796 bp	DNA	linear	PAT 09-JAN-2002
TITLE	AX337968.1	Sequence	9	from Patent	2796 bp	DNA	linear	PAT 09-JAN-2002

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1

Yue H., He A., Nguyen D.B., Yao M.G., Bandman O., Burford N.,

Tang Y.T., Xu Y., Hafalia A., Azimzai Y. and Wallis N.K.

Intracellular signaling proteins



Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.  
NEDO human cDNA sequencing project

TITLE  
JOURNAL  
REFERENCE

2 (bases 1 to 2830)  
Sugano, S., Suzuki, Y., Ota, T., Ohayashi, M., Nishi, T., Isogai, T.,  
Shibahara, T., Tanaka, T. and Nakamura, Y.

TITLE  
JOURNAL

Direct Submission  
Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure, Human Genome  
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: cna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,  
Fax: 81-3-5449-5416)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
Research Association for Biotechnology; cDNA library construction;  
5'- & 3'-end one pass sequencing; Department of Virology and Human  
Genome Center, Institute of Medical Science, University of Tokyo  
(partly supported by Science and Technology Agency).

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CDS

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BASE COUNT  
ORIGIN

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LOCUS					

















\* consists of 75 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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 Job time : 4991 secs

GenCore version 5.1.3

Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 08:26:01 : Search time 2289 seconds

(without alignments)

12561 679 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

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Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs. 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*  
 2: em\_esthum.\*  
 3: em\_estin.\*  
 4: em\_estmu.\*  
 5: em\_estov.\*  
 6: em\_estpl.\*  
 7: em\_estro.\*  
 8: em\_htr.\*  
 9: gb\_est1.\*  
 10: gb\_est2.\*  
 11: gb\_htr.\*  
 12: gb\_est3.\*  
 13: gb\_est4.\*  
 14: gb\_est5.\*  
 15: em\_estfun.\*  
 16: em\_estom.\*  
 17: gb\_gss.\*  
 18: em\_gss\_hum.\*  
 19: em\_gss\_inv.\*  
 20: em\_gss\_pla.\*  
 21: em\_gss\_vrt.\*  
 22: em\_gss\_fun.\*  
 23: em\_gss\_mam.\*  
 24: em\_gss\_mus.\*  
 25: em\_gss\_other.\*  
 26: em\_gss\_pro.\*  
 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1205.2	67.9	1921	11 AK018582	AK018582 Mus muscu
2	1202	67.8	2741	11 AK004847	AK004847 Mus muscu
3	836.8	47.2	1954	11 BC030951	BC030951 Homo sapi
4	680.4	38.4	1806	11 BC012931	BC012931 Homo sapi
5	673.8	38.0	811	13 B1600046	B1600046 603251431
6	654.2	36.9	1000	13 B1600419	B1600419 603246459

7	644.2	36.3	676	10 AV690200	AV690200
8	641	36.1	773	13 B1601096	B1601096
9	623.4	35.1	840	11 AK008312	Mus muscu
10	622.8	35.1	1150	13 B1488609	B1488609
11	622.4	35.1	906	12 BG165370	603246005
12	622.2	35.1	683	10 AV686169	AV686169
13	615.4	34.7	996	12 BG176206	BG176206
14	577	32.5	681	13 B1220592	603233351
15	564.4	31.8	683	10 AV692456	AV692456
16	542.8	30.6	557	13 BM507037	BM507037
17	537.2	30.3	904	12 BF664617	1h4a05.Y
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21	513.8	29.0	841	12 BF663559	602124911
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23	502.2	28.3	872	12 BF699229	602126878
24	499.4	28.2	789	12 BF669635	602120364
25	496	28.0	879	12 BF666897	602121530
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27	482.4	27.2	774	12 BG432146	602496225
28	481.6	27.1	841	12 BF666680	602121368
29	481.6	27.1	847	12 BE958515	601645138
30	475.6	26.8	804	13 B1653069	603300779
31	471.8	26.6	856	12 BE958087	601644929
32	469	26.4	680	10 BE308209	601095109
33	468.6	26.4	884	12 BF542034	602069189
34	466.4	26.3	835	12 BE958350	601644838
35	461.4	26.0	622	12 BF137973	601784651
36	459.2	25.9	725	13 B1557834	603236825
37	458.6	25.9	466	12 BF382058	601816390
38	456.4	25.7	732	12 BF246687	601855477
39	443.6	25.0	813	13 B1648028	602273210
40	442.6	24.9	619	13 BG991456	MRI-H1106
41	441.8	24.9	889	12 BG172246	602333390
42	440	24.8	862	12 BF700761	602128561
43	435.4	24.5	854	12 BF670202	602124352
44	431.4	24.3	759	12 BE958295	601645073
45	427.2	24.1	942	12 BF967109	602287635

## ALIGNMENTS

RESULT 1	AK018582	1921 bp	mRNA	linear	HFC 19-JAN-2002
LOCUS	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130001F19: BRAIN CDNA, CLONE MNCB-3816, SIMILAR TO AF171875 G1-RELATED ZINC FINGER PROTEIN (MUS MUSCULUS), full insert sequence.				
ACCESSION	AK018582				
VERSION	AK018582.1	GI:12858361			
KEYWORDS	HTC: CAP trapper.				
SOURCE	Mus musculus (strain:G57BL/6J) adult male cecum cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci,P. and Hayashizaki,Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
PMID	20494924				





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QY 732 CCATGTCCTCACCCGGGTGAGTACATTTGTTGCAATCATCATCGGCAATCTGAAAGCA 791
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Db 838 TAATTAGCGGCAATCTGGGCTATTATTATCTTTTATCTGCTGAAGGCTAGCAATG 897
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Db 898 CAAAGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 957
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Db 958 AGCTTCAGTCTGACCTTGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1017
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QY 1152 ATATTTTCTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1211
Db 1078 ATATTTTCTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1137
QY 1212 GCAATGTCACATCTCAAGCTTTGCGAATTTGAGGTGGATGTTGAAGATGGATCAGTGT 1271
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QY 1332 ATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1391
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QY 1392 TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1451
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Db 1498 TGAACCATTAAG- TAATAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1557
QY 1629 ATAAATTTTAATAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1688
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# RESULT 2 AK004847 LOCUS DEFINITION

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AF004847.1 GI:12836339  
VERSION  
HTC; CAP trapper.  
KEYWORDS  
Mus musculus (strain:G57BL/6J) adult male liver cDNA to mRNA,  
clone:lib:RIKEN full-length enriched mouse cDNA library  
clone:1300002C13.

## ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
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AUTHORS

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

- AK004847 2741 bp mRNA linear HTC 19-JAN-2002  
Mus musculus adult male liver cDNA, RIKEN full-length enriched  
library, clone:1300002C13:BRAIN CDNA, CLONE MNCB-3816, SIMILAR TO  
AF171875 G1-RELATED ZINC FINGER PROTEIN (MUS MUSCULUS), full insert  
sequence.  
AK004847  
AF004847.1 GI:12836339  
HTC; CAP trapper.  
Mus musculus (strain:G57BL/6J) adult male liver cDNA to mRNA,  
clone:lib:RIKEN full-length enriched mouse cDNA library  
clone:1300002C13.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636  
2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
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3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, M., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watanabe, K.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
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Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
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4  
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
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Baldarelli, P., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,  
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hermann, M., Hume, D. A., Kaniya, M., Lee, N. H., Lyons, P.,  
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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
Teyssie, K. K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlsuki, S.  
and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 406 (6821), 685-690 (2001)  
21085660  
11217851  
5 (bases 1 to 2741)  
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,  
Arakawa, T., Baldarelli, P., Bono, H., Brownstein, M., Bult, C.,  
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BC030951 1054 bp mpNA linear HTC 13-JUN-2002  
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 SOURCE human.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1954)  
 Strausberg, R.  
 Direct Submission  
 Submitted (03-JUN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgaps@rmail.nih.gov](mailto:cgaps@rmail.nih.gov)  
 Tissue procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mdj@paxil.stanford.edu](mailto:mdj@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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 This clone was selected for full length sequencing because it  
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## RESULT 4

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 IMAGE:4456033, mRNA.  
 ACCESSION BC012931  
 VERSION BC012931.1 GI:15277870  
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 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1806)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-AUG-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [villalob@bcm.tmc.edu](mailto:villalob@bcm.tmc.edu)  
 Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,  
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 28 Row: b Column: 9  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA GI: 152440332  
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 /note="Vector: pCMV-SPORT6"  
 BASE COUNT 616 a 266 c 317 g 607 t  
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Query Match 38.4%; Score 680.4; DB 11; Length 1806;  
 Best Local Similarity 98.6%; Pred. No. 1e-148; 7; Indels 3; Gaps 2;  
 Matches 707; Conservative 0; Mismatches 0  
 QY 1358 GGACACAGGAAATGGCCCTGATGGAGATAGTGTCTGTGTGTAATGTATATA 1117  
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 DB 1 GGAGACAGGAAATGGCCCTGATGGAGATAGTGTCTGTGTGTAATGTATATA 60  
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 QY 1118 CCAATGATTTGGTACCACTTTAACTGTGAACCATATTTCCATAGACATGTTGAC 1177  
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 DB 181 GCAATGAGGAGATTTGAATGATGATGATGATGATGATGATGATGATGATGATG 240  
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 QY 1298 ATATGAAATGGCTCTCTCCATGAAGAGGATAATTCGACGAGCGCATCATCTGGA 1357

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 QY 1718 TTAACCTTTTCCACCAAACTCATTAATATATTTTCATAGCAAGTTTCCTCTCAG 1774  
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RESULT 5  
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 LOCUS 811 bp mRNA linear EST 07-SEP-2001  
 DEFINITION G3321431F1 NIH\_MGC\_26 Homo sapiens cDNA clone IMAGE:5303239 5';  
 mRNA sequence.

ACCESSION BI600046  
 VERSION BI600046.1 GI:15492985  
 KEYWORDS EST.  
 SOURCE human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 811)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM1767 Row: n Column: 08  
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## FEATURES

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 /clone="IMAGE:5303239"  
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 /lab\_host="DH10B"

Note=Organ: brain; Vector: pBluescriptP (modified  
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 size-selected for average insert size 2.3 kb and  
 normalized to ROT 5. This is a primary library enriched

for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIMH/NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC Library.  
BASE COUNT 153 a 244 c 264 g 150 t

Query Match 38.0%; Score 673.8; DB 13; Length 811;  
Best Local Similarity 94.2%; Pred. No. 3.3e-147;  
Matches 745; Conservative 0; Mismatches 37; Indels 9; Gaps 4;  
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QY 194 ACCAGGCTCTCTGCCAAGCTCTAGGAGGCGGTGCGCAGGGCGCTAGGGAACCTGGGAGC 253  
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QY 314 TCCAGATTGCTGGCATGTGCTTCTCTGCTGGCGCTGAGTCTGGCAGGACCGCGTTCCCGG 373  
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QY 434 GTGAACCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 493  
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DEFINITION mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BI600419  
BI600419.1 GI:15493358  
EST.  
human.  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 1000)  
NIH-MGC http://mgc.nhl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11730 row: c column: 15  
High quality sequence stop: 701.

FEATURES  
source

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/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptR (modified  
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); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTN-3',  
size-selected for average insert size 2.3 kb and  
normalized to R0T 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIMH/NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC Library."  
BASE COUNT 206 a 299 c 321 g 174 t

Query Match 36.9%; Score 654.2; DB 13; Length 1000;  
Best Local Similarity 93.7%; Pred. No. 1.3e-142;  
Matches 747; Conservative 0; Mismatches 43; Indels 7; Gaps 6;

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Db 82 TACTTGGCACTTCCCGCAGTCTCTCACTCCATTTCTTCCCGCAGCTGGCGGCACTGCTCAAG 141  
QY 194 ATCAAGTCTCTTCCCAAGGCTAGGAGGCGGTGCTGAGGCGGCTAGGGAACCTGGGAGC 253  
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QY 374 GGGGCTGGAAGCAGTGTGGACCGCGTACCTCAACGTTGCTGCTGCGGGTTTCCGACACGGA 433  
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QY 434 GTGAACCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 493  
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RESULT 7
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DEFINITION AV690200 gpc Homo sapiens cDNA clone IMAGE5301380 5', mRNA
ACCESSION AV690200
VERSION AV690200.1 GI:10292063
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homocididae; Homo.
REFERENCE 1 (bases 1 to 676)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Cheng, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26): 15089-15094 (2001)
MEDLINE 21625106
COMMENT Contact: Zequan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source location/Qualifiers
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BASE COUNT 94 a 223 c 231 g 125 t 3 others
ORIGIN

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Db 244 TCCAGATGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
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ACCESSION AV690200
VERSION AV690200.1 GI:15494035
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homocididae; Homo.
REFERENCE 1 (bases 1 to 773)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgab@r-mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

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Db 561 TTGGGCTCATCCAAAGCGGGGGCTGACCTTGGCAACAAGATCCATCTGGCTTAT 620

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 /db\_xref="taxon:9606"  
 /clone="IMAGE:5191785"  
 /clone\_lib="NIH\_MGC\_114"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1. NotI;  
 site 2: EcoRV (destroyed). RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.5 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code: 019. Note:  
 this is a NIH\_MGC Library."  
 264 a 315 c 336 g 235 t

BASE COUNT  
 ORIGIN

Query Match 35.1%; Score 622.8; DB 13; Length 1150;

Best Local Similarity 95.8%; Pred. No. 3.1e-135;

Matches 747; Conservative 0; Mismatches 22; Indels 11; Gaps 10;

QY 174 CTGGCGGCACTGTCTCAGACACAGGGTCTTGGCCAAAGGCGCTAGGAGGGCGCGCTGTCCAGGG 233  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 1 CTGGCGGCGCACTGTCTCAGACACCA-GGTCTCTGCCAAAGGCGCTAGGAGGGCGCGCTGCCA-GG 58  
 QY 234 GCCTAGGCACTGGGAGCGCGCGCGCATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 59 GCCTAGGCACTGGGAGCGCGCGCGCATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 QY 294 GCGCGCGTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 353  
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 119 GCGCGCGTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 174  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 QY 354 CGCAGGCACTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 412  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 179 CGCAGGCACTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 238  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 QY 413 TGGCGCGTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 472  
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 239 TGGCGCGTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 298  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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 299 TAGCGCGGCACTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTG 358  
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 359 GGGCGCGTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 418  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 QY 592 CACCGTGCAAGTCTCTTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATG 651  
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 419 CACCGTGCAAGTCTCTTGGTGGCGCTTTTCAGATTCCTGATGCTGATGCTGATGCTGATGCTGATG 478  
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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 QY 830 ACAATGCTATGAGAGTA-GGGAAGAAACATGGCGCTTGGGCTGATC-ACTATTCAATTT 887  
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 659 ACAATGCTATGAGAGTAGCGGGAAGAAACATGGCGCTTGGGCTGATC-ACTATTCAATTT 718  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 QY 888 TTTTGGCTTC--TGTCCTCTTTTATTATTA-TTACGGCGGCAACTGTGGGCTATTATTATCT 944  
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## RESULT 11

BG165370

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG165370 906 bp mRNA linear EST 06-FEB-2001  
 40244005P1 NIH\_MGC\_94 Homo sapiens cDNA clone IMAGE:4456033 5',  
 mRNA sequence.

BG165370 GI:12672073

BG165370.1

EST.

human.

Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

NIH-MGC http://mgc.nci.nih.gov/.

1 (bases 1 to 906)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10250 row: j column: 02

High quality sequence stop: 649.

Location/Qualifiers

1..906

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4456033"

/clone\_lib="NIH\_MGC\_89"

/tissue\_type="hypernephroma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site: 1. NotI;

site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.3 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

275 a 204 c 183 g 244 t

BASE COUNT

ORIGIN

Query Match 35.1%; Score 622.4; DB 12; Length 906;

Best Local Similarity 96.0%; Pred. No. 3.7e-135;

Matches 692; Conservative 0; Mismatches 22; Indels 7; Gaps 5;

QY 1058 GGAGACAAGAAATGGCCCTGATGGAGATAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1117

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

1 GGAGACAAGAAATGGCCCTGATGGAGATAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 59

QY 1118 CCAATGATTTGGTACGATCTTAACGTGCAACCATATTTTCCATAGACATGTTGCTGAC 1177

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY 1178 CCATGCTGCTTAAACACAAGACTTGCCTCATGTCACATGTCACATGTCACATGTCACATGTCACATG 1237

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

119 CCATGCTGCTTAAACACAAGACTTGCCTCATGTCACATGTCACATGTCACATGTCACATGTCACATG 177

QY 1238 GGAATGAGCTGGATGTTTGAAGATGATCAGTGTCTTTTACAGTCCCTGTATCCAAATGAA 1297

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

178 GGAATGAGCTGGATGTTTGAAGATGATCAGTGTCTTTTACAGTCCCTGTATCCAAATGAA 237

QY 1298 ATATCTAATAGTGCCTCTCCATGAAGAGGATTAATCCACGAGAGCGGATCATCTGGA 1357

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

238 ATATCTAATAGTGCCTCTCCATGAAGAGGATTAATCCACGAGAGCGGATCATCTGGA 247

QY 1358 TATGCTTACAGTACAGGAAACAGATGAACCGCTCTGGAGGAAACACGTCGAGTCACAAAT 1417

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

298 TATGCTTACAGTACAGGAAACAGATGAACCGCTCTGGAGGAAACACGTCGAGTCACAAAT 357



DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LRAM10256 row: f column: 13  
High quality sequence stop: 668.

Db 660 GT -AACCATGAAGCAAAATTCGTGGCGGTGGATGTGTCCCATCTTGACAAACCCAAAC 718

QY 1492 CTTTGAAG -AAGACGAAGAACTCCTTAATCAAGAGACTGTGTTTCGAGAATTAATCTTAAA 1550

Db 719 CTTTGAAGAAGATGAATATCCCTGATCAAGAGACASTGTGTCGGGASATTCACTGTAC 778

QY 1551 ATCTGTGTAATAGAAAACTTGAACCATTTAGTAATAAC 1588

Db 779 ATCTGTGTCATTACAAAATTTGAACCGTGTGTTACACAC 816

RESULT 14	
BI220592	
LOCUS	681 bp mRNA linear EST 11-JUL-2001
DEFINITION	602936079P1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5099346 5', mRNA sequence.
ACCESSION	BI220592
VERSION	BI220592.1 GI:14674036
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 681)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.	Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>		
	Tissue Procurement: Jeffrey E. Green, M.D.	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (tLNL)	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution. MGC clone distribution information can be found through the I.M.A.G.E. Consortium/tLNL at:	<a href="http://image.llnl.gov">http://image.llnl.gov</a>		
	Plate: L1AM11238	row: n	column: 19	
	High quality sequence	stop: 681.		

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FEATURES
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    high quality sequence stop=681.
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        /clone="IMAGE:5099346"
        /clone_lid="NCI_CGAP_Li9"
        /lab_host="DHI0B (71 phage-resistant)"
        /note="Organ: liver; Vector: pCMV-Sport6; Site_1: NotI;
        Site_2: SalI, Cloned unidirectionally. Primer: Oligo dT.
        Average insert size 1.9 kb. Constructed by Life
        Technologies. Note: this is a NCI CGAP library."

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QY	681	CTCTTGGACGGCTATGCTTTAACTTCTCCGGGACCGCAATAGGTCTATCCCATGTCTC	749
Db	241	CTCTTGGACGGCGTATGCTTTAACTTCTCCGGGACCGCAATAGGTCTATCCCATGTCTC	300
QY	741	ACCCGCGGCGTAACTAGATTTGTTGAATCATGATCGGCAATCTGAATGCAACAAAATTG	800
Db	301	ACCCGCGTCTTGGGACATCTTGGCAATCATGATTGGCAATCTGAACAGCAACAAAATTG	360
QY	801	TGCAATCTATTCAAGAGGCAATCAACTACAAATGCTCATAGAATGAGGAAAAAATATG	860
Db	361	TGCAGTCTATTCAAGAGGCGATCAAGTCACAAATGCTCATGGAATAGG--AAACATG	418
QY	861	GGCCTTGGGTC--AATCACTATCAATTTTTCGTTCTGCTGCTCTTTTATTATTACG	919
Db	419	GGCCTTGGGTGAATCATTTATCAATTTCTCGTTCTGCTGCTCTTTTTCATAATTACG	478
QY	920	GGGCAACTGTGGGCTATTTTATCTTTATTTGCTCGAAGCTATCGGAATGCAAGAGCT	979
Db	479	GAAGCAAGTGTGGGCTATTTATCTTTATTTGCTCGAAGATTACGAAATGCAAGAGCT	538
QY	980	CAAAACGAGAAAGAGAGCAATTAAGGCGAGTGTCTAAAAAGCTATTGGGAGGCTTCAA	1039
Db	539	CAAGACAGTAAGAAAGAGGCAATTAAGGCGAGATGCTTAAAAAGCTATTGGAAGCTTAA	598
QY	1040	CTACGCACTGAAACAGGAGACCAAGAAATTTGGCTCTGATGGACATAGTGTGCTGTG	1099
Db	599	CTGCGCACTTGAACAGAGAGCAAGAAATTTGGGCTGATGGAGATAGCTGTGCTGTG	658
QY	1100	TGCATTGAATTGTATAACCCAAA	1122
Db	659	TGCATTGAGCTGTATAACCCAAA	681

RESULT 15	
AV692456	
LOCUS	AV692456 GKCC Homo sapiens cDNA clone GKCCB09 5', mRNA sequence.
DEFINITION	AV692456 GKCC Homo sapiens cDNA clone GKCCB09 5', mRNA sequence.
ACCESSION	AV692456
VERSION	AV692456.1 GI:10294319
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 583)
AUTHORS	Xu,X., Huang,Z., Xu,Z., Qian,R., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Gu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Zhong,M., Xu,S., Gu.W., Huang.W., Zhao.X., Hu.G., Gu.J., Chen.Z. and Han,Z.
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL	Proc Natl Acad Sci U S A 98 (26) :15089-15094 (2001)

BASE COUNT	225 a	127 c	126 g	200 t	5 others
ORIGIN					
Query Match	31.8%	Score 564.4	DB 10	Length 683	
Best Local Similarity	9A 0%	Pred. No. 1.4e-121			
Matches 591	Conservative 0	Mismatches 9	Indels 3	Gaps	
QY	1172	GTGTGCCCATGCGCTGTTAAAAACACAAGACTTGCCTCATGTGCCAAATGTGCATACTCAAA	1231		
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QY	1232	GCTTTGGGAATTGAGGTGGATGTTGCAAGATGGATCAGTGTCTTTTACAAGTCCCTGTATCC	1291		
Db	61	GTCTTTGGGAATTGAGGTGGATGTTGCAAGATGGATCAGTGTCTTTTACAAGTCCCTGTATCC	120		
QY	1292	AATGAATAATCTAAATAGTGCCTGCTCCCATCAAGAGGATAATCGACGGAGACCGCATCA	1351		
Db	121	AATGAATAATCTAAATAGTGCCTGCTCCCATCAAGAGGATAATCGACGGAGACCGCATCA	180		
QY	1352	TCTGGATATGCTTTCAGTACAGGGAACAGATGAACCGCTCTGSGAGGAACACGTGCAGTCA	1411		
Db	181	TCGTGATATGCTTTCAGTACAGGGAACAGATGAACCGCTCTGSGAGGAACACGTGCAGTCA	240		
QY	1412	ACAAATGAAAGTCTTCACGCTGGTAAACCATGAACAAATTCCTGTGGCAGTGGATGTATT	1471		
Db	241	ACAAATGAAAGTCTTCACGCTGGTAAACCATGAACAAATTCCTGTGGCAGTGGATGTATT	300		
QY	1472	CTCTATGCTGTAATGCTTAAATCTGTTAAATAGAAAACCTTGAACCCATTAGTAATAACAGA	1531		
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QY	1532	CGAGAATTTAAATCTTAAATCTGTTAAATAGAAAACCTTGAACCCATTAGTAATAACAGA	1591		
Db	361	CGAGAATTTAAATCTTAAATCTGTTAAATAGAAAACCTTGAACCCATTAGTAATAACAGA	420		
QY	1592	ATTCGCAATCAAGGCGCTAGTTCTTATTAATAAATGSAATAATTTAATAAAATAAGAGTG	1651		
Db	421	ATTCGCAATCAAGGCGCTAGTTCTTATTAATAAATGSAATAATTTAATAAAATAAGAGTG	480		
QY	1652	ATACTGAAAGTGCTCAGATGACTAATATATGCTATAGTTAAATGCTTTAAANAATATTT	1711		
Db	481	ATACTGAAAGTGCTCAGATGACTAATATATGCTATAGTTAAATGCTTTAAANAATATTT	538		
QY	1712	AACCTGTTAACTTTTTTCCACCAAACTCATTAATAATTTTTTCATAGGCAAGTTTCCTCT	1771		
Db	539	AACCTGTTAACTTTTTTCCCA-CAAACTCATTAATAATTTTTTCATAGGCAAGTTTCCTCT	597		
QY	1772	CAG 1774			
Db	598	CAG 600			

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 Job time: 2306 secs

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Job time : 2306 secs

GenCore version 5.1.3

Copyright (c) 1993 - 2002 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 01:30:37 : Search time 360 Seconds  
(without alignments)  
11097.347 Million cell updates/sec

Title: us-09-854-300-7

Perfect score: 1774

Sequence: 1 agctggagctccacggcgt ataggcaatttctctctcag 1774

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1773	99.9	1774	AA172095	Human GRIL cDNA.
2	1662.8	93.7	2773	AA15595	Human protein c10n
3	1662.8	93.7	2796	AA172321	ISIGP-4 cDNA. Hom.
4	1431.4	80.7	2876	AA542511	Human cDNA encoding
5	1278.2	72.1	1284	AA15595	Human protein c10n
6	1178.8	66.4	2306	AA525884	Human cDNA encoding
7	1167.2	65.8	1249	ABL90796	Human polynucleoti
8	1166	65.7	2145	AA172094	Mouse GRIL cDNA.
9	1157.5	65.3	1250	AA526340	Human cDNA encoding

10	1106.8	62.4	1287	24	ABK12983	Mouse goliath cDNA
11	1052.4	59.3	1287	24	ABK12992	Synthetic goliath
12	1042.8	58.8	1287	24	ABK12990	Synthetic goliath
13	1042.8	58.8	1287	24	ABK12991	Synthetic goliath
14	1019.4	57.5	1135	22	AA159292	Human polynucleoti
15	999.6	56.3	1287	24	ABK12989	Synthetic goliath
16	977.2	55.1	1287	24	ABK12987	Synthetic goliath
17	972.4	54.8	1287	24	ABK12988	Synthetic goliath
18	655.2	36.9	737	22	AA161078	Human polynucleoti
19	497.2	28.0	502	24	ABN19991	Human ORFX polynuc
20	392.2	22.1	404	22	AAF66696	Novel human polynu
21	372.6	21.0	646	24	ABL38236	Human colon tumour
22	310	17.5	435	24	ABK45625	cDNA encoding colo
23	254.8	14.4	1355	21	AAAB7765	Human secreted pro
24	254.8	14.4	1355	22	AAF64047	cDNA encoding huma
25	243.8	13.7	918	23	AA570124	DNA encoding novel
26	210.2	11.8	2826	24	ABL90797	Human polynucleoti
27	209	11.8	1200	22	AAF94484	Human hydrophobic
28	209	11.8	1527	22	AAF94454	Human hydrophobic
29	209	11.8	2005	22	AAK94499	Human full-length
30	209	11.8	2063	19	AAV43601	Human secreted pro
31	209	11.8	2452	22	AAK94373	Human full-length
32	194.8	11.0	1869	22	ABA09101	Human secreted pro
33	194.8	11.0	1869	22	AAK51507	Human polynucleoti
34	194.8	11.0	1869	22	AAK52491	Human polynucleoti
35	191.8	10.8	1708	23	AA576863	DNA encoding novel
36	180.8	10.2	3615	24	ABK36205	cDNA sequence #596
37	178.8	10.1	631	21	AACT76002	Human ORFX ORF1557
38	149.2	8.4	1322	19	AAV43616	Human secreted pro
39	148.8	8.4	1260	24	ABK12986	Mouse g1 cDNA sequ
40	147.6	8.3	1253	19	AAV40387	Human zinc binding
41	147.6	8.3	1257	22	AAF94418	Human hydrophobic
42	147.6	8.3	1433	22	AAF94428	Human hydrophobic
43	147.6	8.3	1489	24	ABL55072	Human cDNA sequenc
44	147.6	8.3	1515	24	ABL90798	Human polynucleoti
45	147.6	8.3	1546	24	ABL55094	Human cDNA sequenc

## ALIGNMENTS

## RESULT 1

AA172095

IC AA172095 standard, cDNA; 1774 BP.

XX AA172095;

XX CC-MAP-2002 (first entry)

XX Human GRIL cDNA.

XX Homo sapiens.

XX Murine; human; GRIL; atenuation; tyrosine phosphorylation;

XX antigenic stimulation; interleukin-2; gene therapy; polymorphism, IL-2;

XX anti-immune disease; tumour cell; cancer; transplant rejection; ss.

XX Key

XX Location/Qualifiers

XX CDS

XX 263..1547

XX /\*tag= a

XX /product= "GRIL"

XX WO200185943-A1.

XX 15-NOV-2001.

XX 11-MAY-2001, 2001WO-US15385.

XX 11-MAY-2000, 2000US-203513P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Ford GS, Bloom D, Fatlman CG;

XX



Db 1441 TCAAGCAAAATCTGTGGCAGTGATGTTATTTCTCATGTGNSACACCCACCTTTGAGA 1500  
 QY 1501 AGACAAACTCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAAATCTGTGTAA 1560  
 Db 1501 AGACAAACTCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAAATCTGTGTAA 1560  
 QY 1561 ATAGAAAACCTTGAACCATTTAGTAATAACAGAACTGCCAATCAGGGCTAGTTTCTATTAA 1620  
 Db 1561 ATAGAAAACCTTGAACCATTTAGTAATAACAGAACTGCCAATCAGGGCTAGTTTCTATTAA 1620  
 QY 1621 TAAATGGATTAATTTAATAAATAGAGAGTACTGAAAGTCTCTCAGATGACTAATATT 1680  
 Db 1621 TAAATGGATTAATTTAATAAATAGAGAGTACTGAAAGTCTCTCAGATGACTAATATT 1680  
 QY 1681 ATGCTATAGTTAAATGCGTTAAATATTTAACTTTTAACTTTTCCACCAACTCA 1740  
 Db 1681 ATGCTATAGTTAAATGCGTTAAATATTTAACTTTTAACTTTTCCACCAACTCA 1740  
 QY 1741 TTATAATATTTTTCATAGGCAAGTTTCTCTCAG 1774  
 Db 1741 TTATAATATTTTTCATAGGCAAGTTTCTCTCAG 1774

RESULT 2  
 ID AAA15995  
 XX AAA15995 standard; cDNA; 2773 BP.  
 AC AAA15995;  
 XX  
 DT 12-JUN-2000 (first entry)  
 XX  
 DE Human protein clone HPI0574 full length coding sequence.  
 KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;  
 KW cytokine production; cell proliferation; cell differentiation;  
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;  
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;  
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;  
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;  
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;  
 KW coagulation disorder; myocardial infarction; inflammatory condition;  
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;  
 KW nephritis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200005367-A2.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 22-JUL-1999; 99WO-3P03929.  
 XX  
 PP 24-JUL-1998; 98JP-0208920.  
 PP 07-AUG-1998; 98JP-0224105.  
 PR 25-AUG-1998; 98JP-0238116.  
 PR 09-SEP-1998; 98JP-0254736.  
 PR 29-SEP-1998; 98JP-0275505.  
 XX  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 XX  
 PI Kato S, Kimura T;  
 XX  
 DR WPI: 2000-182694/16.  
 DR P-PSDB: AAY94897.  
 XX  
 PT Novel human proteins having hydrophobic domains useful for treating  
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,  
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -  
 XX  
 PS Claim 4; Page 348-351; 351pp; English.  
 XX

CC This sequence encodes a human protein of the invention, which has  
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a  
 CC genetic marker. The protein can also be used as a marker, and to identify  
 CC potential genetic disorders. The DNA and protein can also be used as  
 CC nutritional sources or supplements. The protein exhibits cytokine, cell  
 CC proliferation, cell differentiation activities and induces production of  
 CC other cytokines in certain cell populations. The protein also exhibits  
 CC immune stimulating or immune suppressing activity. It can be used in the  
 CC treatment of various immune deficiencies and disorders, and to treat  
 CC infectious diseases caused by viral, bacterial, fungal or other  
 CC infections. The protein is also used for treating autoimmune disorders  
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid  
 CC arthritis. It is also useful in the treatment of allergic reactions and  
 CC conditions such as asthma, and in immune suppression after organ  
 CC transplantation. The protein is useful in regulation of haematopoiesis  
 CC and consequently in the treatment of myeloid or lymphoid cell  
 CC deficiencies. It is also used in compositions for tissue growth or  
 CC regeneration. The protein is also used in the treatment of osteoporosis  
 CC or osteoarthritis and in the treatment of periodontal disease and other  
 CC tooth repair processes. The protein is used in the treatment of nervous  
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and  
 CC Huntington's disease. They are useful for protection or regeneration and  
 CC treatment of lung or liver fibrosis, reperfusion injury in various  
 CC tissues, and conditions resulting from systemic cytokine damage. They are  
 CC also used for promoting or inhibiting tissue differentiation. They are  
 CC also used as contraceptives since they exhibit activin or inhibin related  
 CC activities and as a fertility inducing therapeutic. They are used for  
 CC treating various coagulation disorders and in treatment and prevention of  
 CC conditions resulting from coagulation activities e.g. myocardial  
 CC infarction or stroke. They also acts as receptors, receptor ligands or  
 CC inhibitors or agonists of receptor/ligand interactions. They are used to  
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia  
 CC reperfusion injury, arthritis, and nephritis. They can be used to  
 CC prevent tumours.  
 XX

SQ Sequence 2773 BP: 803 A: 545 C: 617 G: 808 T: 0 other;

Query Match 93.7%; Score 1662.8; DB 21; Length 2773;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1690; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 74 CCGAGGAGCTGCATCTCTGGGCAACCTGTGTGTGAGCGTACGTGCTCTCTGCTCGGAGC 133  
 Db 22 CCGAGGAGCTGCATCTCTGGGCAACCTGTGTGTGAGCGTACGTGCTCTCTGCTCGGAGC 81

QY 134 TAGCTCGAGCTCCCACTCTCACTCCATCTCTCCCACTCTGGCGGCGACCTGCTCAAG 193  
 Db 82 TAGCTCGAGCTCCCACTCTCACTCCATCTCTCCCACTCTGGCGGCGACCTGCTCAAG 141

QY 194 ACTAGGGCTCTCTGCTCAAGCGCTAGGAGGGGGGGTGGAGGGGGGGTGGAGGGGGGGG 253  
 Db 142 ACTAGGGCTCTCTGCTCAAGCGCTAGGAGGGGGGGTGGAGGGGGGGTGGAGGGGGGGG 201

QY 254 GCGGG 313  
 Db 262 GCGGG 261

QY 314 TCCAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373  
 Db 262 TCCAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321

QY 374 GGGGCTGAATCTAGTGTGGAGCGGTACCTCAAGTCTGCTGGGGGGGGTTCGACACGGGA 433  
 Db 322 GGGGCTGAAGCAGTGTGGAGCGGTACCTCAAGTCTGCTGGGGGGTTCGACACGGGA 381

QY 434 GTGAACCGTACGTGTGGAGCGGTACGTGGAGGGGGGGTGTACGGCCAGGACTCGCGGCTG 493  
 Db 382 GTGAACCGTACGTGTGGAGCGGTACGTGGAGGGGGGGTGTACGGCCAGGACTCGCGGCTG 441

QY 494 GAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553  
 Db 442 GAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501





```
QY 134 TAGCTCGACGCTCCCGAGTCTCAGTCCATTCCTCCACGCTGGCGGCCACCTGCTCAAG 193
DB 1168 AATGTGACATACCTCAAGAGCTTTGGGAATTGAGGTGGATGTTGAAGATGGATGATGCT 1273
DB 1168 AATGTGACATACCTCAAGAGCTTTGGGAATTGAGGTGGATGTTGAAGATGGATGATGCT 1227
QY 1274 TTACAGTCCCTGTATCCCAATGAAATATCTAATAGTGCCTCTCCCATGAAGAGATAAT 1333
DB 1228 TTACAGTCCCTGTATCCCAATGAAATATCTAATAGTGCCTCTCCCATGAAGAGATAAT 1287
QY 1334 CGCAGGACACGTCGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCGCTCTG 1393
DB 1288 CGCAGGACACGTCGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCGCTCTG 1347
QY 1394 GAGGAACACGTCGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCGCTCTG 1453
DB 1348 GAGGAACACGTCGATCATCTGGATATGCTTCAGTACAGGGAACAGATGAACCGCTCTG 1407
QY 1454 GTGGCAGTGGATGTTATTTCCTCATGTGACACCAACCTTTGAAGAGAGCAAACTCT 1513
DB 1408 GTGGCAGTGGATGTTATTTCCTCATGTGACACCAACCTTTGAAGAGAGCAAACTCT 1467
QY 1514 AATCAAGAGACGTCGTCGAGAAATTAATCTTAAATCTGTGTAAATAGAAACTTGA 1573
DB 1468 AATCAAGAGACGTCGTCGAGAAATTAATCTTAAATCTGTGTAAATAGAAACTTGA 1527
QY 1574 ACCATTAGTAATAACAGAACTGCCAATCAGGCGCTAGTTCTTAAATAGGATAA 1633
DB 1528 ACCATTAGTAATAACAGAACTGCCAATCAGGCGCTAGTTCTTAAATAGGATAA 1587
QY 1634 TTTAATAAATAAGAGTGATGATGAAAGTGTGATGATGATGATGATGATGATGATGAT 1693
DB 1588 TTTAATAAATAAGAGTGATGATGAAAGTGTGATGATGATGATGATGATGATGATGAT 1647
QY 1694 AATGCTTAAATATTTAACTGTAACTTTTCCACCAACTCATTATAATATTTT 1753
DB 1648 A--TGCTTAAATATTTAACTGTAACTTTTCCCA--CAACTCATTATAATATTTT 1704
QY 1754 CATAGCAAGTTTCTCTCAG 1774
DB 1705 CATAGCAAGTTTCTCTCAG 1725

RESULT 4
AAS42511
ID AAS42511 standard: cDNA: 2876 BP.
XX
AC AAS42511;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding an mddt protein, clone LI:757439.1:2000MAY01.
XX
KW Human: molecules for disease detection and treatment; mddt; ss;
KW Antiarteriosclerotic; hepatotropic; antipsoriatic; cytostatic;
KW immunosuppressive; antidiabetic; antineoplastic; neuroprotective;
KW osteopathic; antirheumatic; cell proliferative disorder;
KW arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
KW leukemia; breast cancer; autoimmune disorder; AIDS;
KW acquired immunodeficiency syndrome; Addison's disease;
KW diabetes mellitus; asthma; multiple sclerosis; osteoarthritis.
XX
OS Homo sapiens.
XX
PN WO200162922-A2.
XX
PD 30-AUG-2001.
XX
PF 21-FEB-2001; 2001WO-US05896.
XX
PR 24-FEB-2000; 2000US-0185213.
PR 16-MAY-2000; 2000US-0205232.
PR 17-MAY-2000; 2000US-0205285.
PR 17-MAY-2000; 2000US-0205286.
PR 17-MAY-2000; 2000US-0205287.
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QY 134 TAGCTCGACGCTCCCGAGTCTCAGTCCATTCCTCCACGCTGGCGGCCACCTGCTCAAG 193
DB 88 TAGCTCGACGCTCCCGAGTCTCAGTCCATTCCTCCACGCTGGCGGCCACCTGCTCAAG 147
QY 194 ACCAGGCTGCTGCCAAGCCTAGGAGGCGCTGCCAGGGCGCTAGGGAACCTGCGGAGC 253
DB 148 ACCAGGCTGCTGCCAAGCCTAGGAGGCGCTGCCAGGGCGCTAGGGAACCTGCGGAGC 207
QY 254 GCGCGGCCATGGGCGCGCGCTGGGCGCGGGGTCTCTGCGCGGGTGGCTGGGCTTT 313
DB 208 GCGCGGCCATGGGCGCGCGCTGGGCGCGGGGTCTCTGCGCGGGTGGCTGGGCTTT 267
QY 314 TCCAGATTGCTGGCATGCTGCTTCTCTGCTGGCCCTGAGTCCGCGAGCACCGGCTCCGG 373
DB 268 TCCAGATTGCTGGCATGCTGCTTCTCTGCTGGCCCTGAGTCCGCGAGCACCGGCTCCGG 327
QY 374 GGGGCTGAGACAGTGTGGACCCGCTACGCTCAACGCTGCTGCGGGGTTCCGCAACCGGA 433
DB 328 GGGGCTGAGACAGTGTGGACCCGCTACGCTCAACGCTGCTGCGGGGTTCCGCAACCGGA 387
QY 434 GTCAACGCTACGCTGGGAGCTGAGCGAGGAGGCGGTGACGGCCAGGACTCCGCGCTG 493
DB 388 GTCAACGCTACGCTGGGAGCTGAGCGAGGAGGCGGTGACGGCCAGGACTCCGCGCTG 447
QY 494 GAGCCTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
DB 446 GAGCCTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507
QY 554 CCGCACAGCAATTTACGCTGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
DB 508 CCGCACAGCAATTTACGCTGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 567
QY 614 GCCTCATCAACGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
DB 568 GCCTCATCAACGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
QY 674 AGATGGCGCTGTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
DB 628 AGATGGCGCTGTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687
QY 734 ATGCTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 793
DB 688 ATGCTTCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
QY 794 AAAATTCTGCAATCTATTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
DB 748 AAAATTCTGCAATCTATTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 807
QY 854 AAACATGCGCTTGGGTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 913
DB 808 AAACATGCGCTTGGGTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 867
QY 914 ATTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
DB 868 ATTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 927
QY 974 AGAGCTCAAGCAGGAGCAGAGGCAATTAAGAGGCAATTAAGAGGCAATTAAGAGGCAAT 1033
DB 928 AGAGCTCAAGCAGGAGCAGAGGCAATTAAGAGGCAATTAAGAGGCAATTAAGAGGCAAT 987
QY 1034 CTTCACTACGCTACACTGAACCAAGAGACCAAGCAATTTGGCTGTGATGATGATGATGAT 1093
DB 988 CTTCACTACGCTACACTGAACCAAGAGACCAAGCAATTTGGCTGTGATGATGATGATGAT 1047
QY 1094 GCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1153
DB 1048 GCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
QY 1154 ATTTTCCATAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1213
DB 1108 ATTTTCCATAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1167
```



















Matches 1208; Conservative 0; Mismatches 10; Indels 5; Gaps 4:

QY 547 CTGTAACCCGACACGAATTTACGCGTCCACGGTTTGGGGAAGACCGGCGCAAGTCTC 606  
 Db 18 CTGTAACCCGACACGAATTTACGCGTCCACGGTTTGGGGAAGACCGGCGCAAGTCTC 77  
 QY 607 TTGGTTGGGCTTCATCAAGCGGCGGCGGCGGCTGCGACCTTGGCAGACAAGATCCCATCTGCG 666  
 Db 78 TTGGTTGGGCTTCATCAAGCGGCGGCGGCGGCTGCGACCTTGGCAGACAAGATCCCATCTGCG 137  
 QY 667 TTATGAGACATGGGCTCTGGAGCTGCTCATCTTTTAACCTCCCGGAGACCCGCAATGAGGT 726  
 Db 138 TTATGAGAGAGGGGCTCTGGAGCGGCTCATCTTTTAACCTCCCGGAGACCCGCAATGAGGT 197  
 QY 727 CATCCCATGCTCTACCCGCGGCTGAGTAGACATTTGTCATCATATGAGTATGAGTATGAGTAA 786  
 Db 198 CATCCCATGCTCTACCCGCGGCTGAGTAGACATTTGTCATCATATGAGTATGAGTAA 747  
 QY 787 AGGCAACAAAATTTCTCAATCTTATTCAGAGAGCGCATACAGTGCATAGAGT 846  
 Db 258 AGGCAACAAAATTTCTCAATCTTATTCAGAGAGCGCATACAGTGCATAGAGT 817  
 QY 847 AGGCAACAAAATTTCTCAATCTTATTCAGAGAGCGCATACAGTGCATAGAGT 905  
 Db 318 AGGCAACAAAATTTCTCAATCTTATTCAGAGAGCGCATACAGTGCATAGAGT 977  
 QY 906 TTTTATTTATAGCGGCGCACTGTGGGCTATTTTATCTTTATCTCTCGAAGGCTAC 965  
 Db 378 TTTTATTTATAGCGGCGCACTGTGGGCTATTTTATCTTTATCTCTCGAAGGCTAC 437  
 QY 966 GGAATCGACAGAGCTCAAGCAGAGAGAGCGAGCGCAATTTAAGCGAGATGCTAAAAAGCTA 1025  
 Db 438 GGAATCGACAGAGCTCAAGCAGAGAGAGAGCGAGCGCAATTTAAGCGAGATGCTAAAAAGCTA 497  
 QY 1026 TTGGAAGGCTTCAACTACGCACACTGAAACAAGAGAGCAAGG-AAATTTGGCGCTGATGGA 1084  
 Db 498 TTGGAAGGCTTCAACTACGCACACTGAAACAAGAGAGCAAGG-AAATTTGGCGCTGATGGA 557  
 QY 1085 GATAGTTGCTGTGTGCAATTTGAATGTATAACCAATGATTTGGTACGCATCTTAACG 1144  
 Db 558 GATAGTTGCTGTGTGCAATTTGAATGTATAACCAATGATTTGGTACGCATCTTAACG 617  
 QY 1145 TGCAACCATATTTCCATAAGACATGCTTGACGCTATGCTTTAAACACACACACTTGC 1204  
 Db 618 TGCAACCATATTTCCATAAGACATGCTTGACGCTATGCTTTAAACACACACACTTGC 677  
 QY 1205 CCATGTGCAAAATGTGACATCTCAAAAGCTTTGGGAATTTGAGTGTGATGTTGAAGATGGA 1264  
 Db 678 CCATGTGCAAAATGTGACATCTCAAAAGCTTTGGGAATTTGAGTGTGATGTTGAAGATGGA 737  
 QY 1265 TCAGTGTCTTTACAGTCTGCTATCCCAATGAATATCTATAGTGGCTCTCCCATGAA 1324  
 Db 738 TCAGTGTCTTTACAGTCTGCTATCCCAATGAATATCTATAGTGGCTCTCCCATGAA 797  
 QY 1325 GAGGATAATCGGAGCAGACCGCATCATCTGATATGCTTCAGTACAGGGAACAGATGAA 1384  
 Db 798 GAGGATAATCGGAGCAGACCGCATCATCTGATATGCTTCAGTACAGGGAACAGATGAA 857  
 QY 1385 CCGCCTCTTGAGAAACATGCAAGTCAACAATGAAGTCTACAGCTGGTAAACCATGAA 1444  
 Db 858 CCGCCTCTTGAGAAACATGCAAGTCAACAATGAAGTCTACAGCTGGTAAACCATGAA 917  
 QY 1445 GCAATCTCTGGCAGTGAATGTTATCTCATGTNGACACCCCAACCTTTGAGAGAC 1504  
 Db 918 GCAATCTCTGGCAGTGAATGTTATCTCATGTGTCACAACTTGAAGAGAGAC 977  
 QY 1505 GAAACTCTTAATCAAGAGACTGCTGTCGAGAAATTTAAATCTTAAATCTGTGTAATAG 1564  
 Db 978 GAAACTCTTAATCAAGAGACTGCTGTCGAGAAATTTAAATCTTGTGTAATAG 1037  
 QY 1565 AAACTTGACCATTTAGTAATAACAGAACTGCTAATTAAGAGAGTGTATTTATTAATAA 1624  
 Db 1038 AAACTTGACCATTTAGTAATAACAGAACTGCTAATTAAGAGAGTGTATTTATTAATAA 1697

QY 1625 TTGCATAAATTTAATAAATAAGACTGATAGTAAGTCTCAGATGACTAATATTATGTC 1684  
 Db 1098 TTGCATAAATTTAATAAATAAGACTGATAGTAAGTCTCAGATGACTAATATTATGTC 1157  
 QY 1685 TATAGTTAAATTTGGCTTTAAATAATTTTAACTGTTTAACTTTTTTCCACCAAACTCATTAT 1744  
 Db 1158 TATAGTTAA--TGCTTTAAATAATTTTAACTGTTTAACTTTTTTCCCA--CAAACTCATTAT 1214  
 QY 1745 AATATTTTTCATAGGCAAGTTTC 1767  
 Db 1215 AATATTTTTCATAGGCAATTTCC 1237

## RESULT 10

ABK12983

ID ABK12983 standard. cDNA, 1287 BP.

XX ABK12983;

XX AC AC

XX DT 23-APR-2002 (first entry)

XX Mouse goliath cDNA sequence.

DE Mouse; goliath protein; antiangiogenic; vasotropic; gene therapy;  
 KW dosage form; angiogenesis; neurogenesis; tumour; vascularisation;  
 KW cancer; ischaemia; neuroblastoma; neurodegenerative disease;  
 KW unrecovered nerve trauma; gene; ss.

XX Mus sp.

XX Key Location/Qualifiers  
 FH 1.1287  
 FT CDS  
 FT /\*tag= a  
 FT /product= "Mouse\_goliath\_protein"

XX WO2001093681-A1.

XX 13-DEC-2001.

XX 01-JUN-2001; 2001WO-US18000.

XX 02-JUN-2000; 2000US-0586398.

XX (REGC ) UNIV CALIFORNIA.

XX Harland R, Baker JC;

XX WPI, 2002-147637/19.

XX P-PSDB; AA074918.

XX New combinations comprising goliath proteins, useful for modulating  
 PT angiogenesis or neurogenesis in mammals e.g. for preventing or  
 PT treating undesirable vascularisation of a tumour, ischaemia or  
 PT neurodegenerative disease  
 XX

FS Examples, Page 38, 45pp, English.

XX The present invention relates to a new pharmaceutical composition that  
 CC comprises a goliath polypeptide in dosage form. The goliath polypeptide  
 CC has a sequence identity of at least 75% to the protein sequences  
 CC (AAU74918-AAU74921) fully defined in the specification. The composition  
 CC is useful for modulating angiogenesis or neurogenesis in mammals,  
 CC particularly in humans or mice. Specifically, the composition is useful  
 CC for the prophylactic and/or therapeutic treatment of excess angiogenesis  
 CC e.g. undesirable vascularisation of a tumour or insufficient angiogenesis  
 CC e.g. ischaemia, excess neurogenesis e.g. neuroblastoma or insufficient  
 CC neurogenesis e.g. neurodegenerative disease or unrecovered nerve trauma.  
 CC The present nucleic acid sequence encodes the mouse goliath protein  
 CC that was used in the invention for modulating angiogenesis or  
 CC neurogenesis.

XX Sequence 1287 BP, 308 A; 320 C; 359 G; 300 T; 0 other;















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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 09:55:20 Search time 115 seconds

(without alignments)  
5139.275 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctggagctccaccgcggt.... ataggcaagtttctctctcag 1774

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 310279 seqs, 166577418 residues

Total number of hits satisfying chosen parameters: 620558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published\_Applications\_NA:\*

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- 11: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB seq:\*
- 12: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB seq:\*
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- 14: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1157.6	65.3	1250	10	US-09-764-864-519
3	372.6	21.0	643	9	US-10-046-935-1815
C 4	310	17.5	435	10	US-09-920-300A-1176
C 5	310	17.5	435	12	US-10-033-528-1176
6	274.6	15.5	387	10	US-09-983-965-5551
7	214.4	12.1	374	10	US-09-983-965-4662
8	209	11.8	2063	10	US-09-935-390A-1
9	202.2	11.3	332	10	US-09-983-965-5467
10	187.4	10.6	340	10	US-09-783-590-3523
11	149.2	8.4	1322	10	US-09-935-390A-16
12	132.6	7.5	619	10	US-09-764-864-485
13	117.2	6.6	463	10	US-09-864-761-11364
C 14	112.8	6.4	826	10	US-09-822-849A-90
15	112.4	6.3	435	10	US-09-983-965-5076
16	105.6	6.0	382	10	US-09-815-343-1328
17	105.2	5.9	253	10	US-09-864-761-27944
18	86.4	4.9	922	10	US-09-803-729-23
19	78.8	4.4	570	10	US-09-734-017A-7

C 20	78.6	4.4	439	10	US-09-925-299-484	Sequence 484, App
C 21	77.4	4.4	2244	10	US-09-764-870-222	Sequence 222, App
C 22	76.8	4.3	1355	10	US-09-764-870-182	Sequence 182, App
C 23	76.8	4.3	1355	10	US-09-764-853-404	Sequence 404, App
24	76	4.3	1772	10	US-09-764-853-148	Sequence 148, App
25	75.6	4.3	496	10	US-09-925-301-686	Sequence 686, App
26	75.6	4.3	1906	10	US-09-739-254-32	Sequence 32, Appl
27	75.6	4.3	1906	10	US-09-904-615-32	Sequence 32, Appl
28	75.2	4.2	618	10	US-09-764-853-377	Sequence 377, App
29	75.2	4.2	618	10	US-09-764-898-126	Sequence 126, App
30	75.2	4.2	2330	10	US-04-764-853-184	Sequence 184, App
31	75	4.2	869	10	US-09-764-864-289	Sequence 289, App
32	75	4.2	2751	10	US-09-789-561-64	Sequence 64, Appl
33	75	4.2	2751	10	US-09-925-301-273	Sequence 273, App
34	74.8	4.2	631	10	US-09-908-711-29	Sequence 29, Appl
35	74.8	4.2	640	10	US-09-908-711-28	Sequence 28, Appl
36	74.8	4.2	796	10	US-09-764-853-365	Sequence 365, App
37	74.8	4.2	1454	10	US-09-764-864-91	Sequence 91, Appl
38	74.6	4.2	2005	10	US-09-764-903-22	Sequence 22, Appl
39	74.4	4.2	791	10	US-09-764-853-305	Sequence 305, App
40	74.4	4.2	852	10	US-09-764-898-50	Sequence 50, Appl
C 41	74.4	4.2	852	10	US-09-764-898-123	Sequence 123, App
42	74.4	4.2	1190	10	US-09-410-194-14	Sequence 14, Appl
43	74.4	4.2	1712	10	US-09-925-300-643	Sequence 643, App
C 44	74	4.2	404	10	US-09-969-708-61	Sequence 61, Appl
45	74	4.2	737	10	US-09-764-853-172	Sequence 172, App

#### ALIGNMENTS

RESULT 1  
US-09-764-864-63  
Sequence 63, Application US/09764864  
Patent No. US6,031,375A1  
GENERAL INFORMATION:  
APPLICANT: Posen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PT223  
CURRENT APPLICATION NUMBER: US/09/764,864  
PRIORITY FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 1792  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 63  
LENGTH: 2306  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-764-864-63

Query Match 66.4%, Score 1178.8, DB 10, Length 2306;  
Best Local Similarity 99.0%, Pred. No. 4.9e-294;  
Matches 1217; Conservative 0; Mismatches 8; Indels 4; Gaps 3;

QY	547	CTGTAACTCCGACACAGTAATTTTACCGTGGCCACGCTTTGGGGAAGACACCGGCAAGCTCTC	606
DB	12	CTGTAACTCCGACACAGTAATTTTACCGTGGCCACGCTTTGGGGAAGACACCGGCAAGCTCTC	71
QY	607	TTGGTTGGGCTTCATCCCAACGCGCGGGGCTGACCTTCGACAGAGATCCCATCTGGC	666
DB	72	TTGGTTGGGCTTCATCCCAACGCGCGGGGCTGACCTTCGACAGAGATCCCATCTGGC	131
QY	667	TTATAGAGATGGGAGTTTGGAG	726
DB	132	TTATAG	191
QY	727	CATCCCATCTCTCACCCCGGGTGGCAGTATGATTTTTCATCATGATGATGATGATGATGATGATG	786
DB	192	CATCCCATCTCTCACCCCGGGTGGCAGTATGATTTTTCATCATGATGATGATGATGATGATGATG	251
QY	787	AGGCAAAATTTCTGCAATCTATTCAAGAGGACATACAGTACAGTACAGTACAGTACAGTACAGT	846
DB	252	AGGCAAAATTTCTGCAATCTATTCAAGAGGACATACAGTACAGTACAGTACAGTACAGTACAGT	311

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QY 847 AGGCAAAACATGGGCGCTGGGTGAATCACTATTCAA-TTTTTTCTGTGTGTCT 905
Db 312 AGGAAACATGGGCGCTGGGTGAATCACTATTCAA-TTTTTTCTGTGTGTCT 371
QY 906 TTTTATTATTAAAGGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 965
Db 372 TTTTATTATTAAAGGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 431
QY 966 GGAATGCAAGAGTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 1025
Db 432 GGAATGCAAGAGTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 491
QY 1026 TTGAAAGGCTTCAACTAGGCAACTGAAACAAAGGCAAGGCAAGGCAAGGCA 1085
Db 492 TTGAAAGGCTTCAACTAGGCAACTGAAACAAAGGCAAGGCAAGGCAAGGCA 551
QY 1086 ATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1145
Db 552 ATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
QY 1146 GCAACCATATTTTCCATAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1205
Db 612 GCAACCATATTTTCCATAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
QY 1206 CCACTGTCAAAATGTGATCACTCAAAAGCTTTTGGGAAATTTGAAGATGAT 1265
Db 672 CCACTGTCAAAATGTGATCACTCAAAAGCTTTTGGGAAATTTGAAGATGAT 731
QY 1266 CAGTGTCTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1325
Db 732 CAGTGTCTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
QY 1326 AGGTAATTTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 1385
Db 792 AGGTAATTTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 851
QY 1386 CGGCTCTTGGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1445
Db 852 CGGCTCTTGGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 911
QY 1446 CAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1505
Db 912 CAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
QY 1506 AAATCTCTAATCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1565
Db 972 AAATCTCTAATCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1031
QY 1566 AAATCTCTAATCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1625
Db 1032 AAATCTCTAATCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1091
QY 1626 TGGTAATTTTAAATTAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1685
Db 1092 TGGTAATTTTAAATTAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1151
QY 1686 ATAGTTAAATTTGCTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1745
Db 1152 ATAGTTAAATTTGCTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1209
QY 1746 ATATTTTTCATAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1774
Db 1209 ATATTTTTCATAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1237
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## RESULT 2

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US-09-764-864-519
; Sequence 519, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

FILE REFERENCE: PT223

CURRENT APPLICATION NUMBER: US/09/764,864

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1792

SOFTWARE: Patent In Ver 2.0

SEQ ID NO 519

LENGTH: 1250

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (540)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (1242)

OTHER INFORMATION: n equals a,t,g, or c

US-09-764-864-519

Query Match 65.3%; Score 1157.6; DB 10; Length 1250;

Best Local Similarity 98.8%; Pred. No. le-288;

Matches 1268; Mismatches 10; Indels 5; Gaps 4;

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QY 547 CTCTAAATTTGCAACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 606
Db 18 CTCTAAATTTGCAACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 77
QY 607 TTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
Db 78 TTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 137
QY 667 TTATGAGAGATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 726
Db 138 TTATGAGAGATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 197
QY 727 CATCTCCATGTCTCCATCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 786
Db 198 CATCTCCATGTCTCCATCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 257
QY 787 AGGCACAAAATTTCTGCAATCTATTCAAGAGGCAAGGCAAGGCAAGGCAAG 846
Db 258 AGGCACAAAATTTCTGCAATCTATTCAAGAGGCAAGGCAAGGCAAGGCAAG 317
QY 847 AGGCAAAAATTTCTGCAATCTATTCAAGAGGCAAGGCAAGGCAAGGCAAG 905
Db 418 AGGCAAAAATTTCTGCAATCTATTCAAGAGGCAAGGCAAGGCAAGGCAAG 377
QY 906 TTTTATTATTAAAGGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 965
Db 378 TTTTATTATTAAAGGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 437
QY 966 GGAATGCAAGAGTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 1025
Db 438 GGAATGCAAGAGTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 497
QY 1026 TTGAAAGGCTTCAACTAGGCAACTGAAACAAAGGCAAGGCAAGGCAAGG 1084
Db 498 TTGAAAGGCTTCAACTAGGCAACTGAAACAAAGGCAAGGCAAGGCAAGG 557
QY 1086 ATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
Db 558 ATAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 617
QY 1145 TGGTAATTTTAAATTAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1204
Db 618 TGGTAATTTTAAATTAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 677
QY 1205 CCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1264
Db 678 CCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 737
QY 1265 TCAGTGTCTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1324
Db 738 TCAGTGTCTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 797
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Db 738 TCAGTGTCTTTACAGTCCCTGTATCAATGAATATCTAATAGTGCCTCCTCCCATGAA 797
QY 1325 GAGGATATCGCAGGAGACCGCATCATCTGGATATGCTTCAGTACAGGGAACAGATGAA 1384
Db 798 GAGGATATCGCAGGAGACCGCATCATCTGGATATGCTTCAGTACAGGGAACAGATGAA 857
QY 1385 CCGGCTCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTACAGTGTGTAACCATGAA 1444
Db 858 CCGGCTCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTACAGTGTGTAACCATGAA 917
QY 1445 GCAAAATCTGTGGAGTGGATGTTATTCCTCATGNGNSAACCCCAACCTTTGAAAGAAC 1504
Db 918 GCAAAATCTGTGGAGTGGATGTTATTCCTCATGNGNSAACCCCAACCTTTGAAAGAAC 977
QY 1505 GAAACTCCTAATCAAGAGACTCTGTGTCGAGAAATTAATCTTAAATCTGTGTAATAG 1564
Db 978 GAAACTCCTAATCAAGAGACTCTGTGTCGAGAAATTAATCTTAAATCTGTGTAATAG 1037
QY 1565 AAAACTTGAACCTATTAGTAATAACAGAACTGCAACTCAGGCGCTAGTTTCTATTATAAA 1624
Db 1038 AAAACTTGAACCTATTAGTAATAACAGAACTGCAACTCAGGCGCTAGTTTCTATTATAAA 1097
QY 1625 TTGATATAATTTAATAAATAAGAGTACTGAAAGTCTCAGATGACTAATATATGCG 1684
Db 1098 TTGATATAATTTAATAAATAAGAGTACTGAAAGTCTCAGATGACTAATATATGCG 1157
QY 1685 TATAGTTAAATGGCTTAAATATTTAACTGTTAACTTTTTCACCAAACTCATAT 1744
Db 1158 TATAGTTAAATGGCTTAAATATTTAACTGTTAACTTTTTCACCAAACTCATAT 1214
QY 1745 AATATTTTTCATAGGCAAGTTTC 1767
Db 1215 AATATTTTTCATAGGCAAGTTTC 1237

RESULT 3
US-10-046-935-1815
; Sequence 1815, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046 935
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1815
; LENGTH: 643
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 584
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1815

Query Match 21.0%, Score 372.6, DB 2, Length 643,
Best Local Similarity 98.0%, Pred. No. 1.5e-86;
Matches 398; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 1369 ACAGGGAACAGATGAACCGCTCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTACA 1428
Db 1 ACAGGGAACAGATGAACCGCTCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTACA 60
QY 1429 GCTGCTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCCTCATGNGNSAACCC 1488
Db 61 GCTGCTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCCTCATGNGNSAACCC 120
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QY 1489 AACCTTTGAAGAGAGAGAAACCTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 1548
Db 121 AACCTTTGAAGAGAGAGAAACCTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 180
QY 1549 AAATCTGTGTAAATAGAAAACCTTGAACCATTTAGTATAACAGAACTGCAACTCAGGCGCT 1608
Db 181 AAATCTGTGTAAATAGAAAACCTTGAACCATTTAGTATAACAGAACTGCAACTCAGGCGCT 240
QY 1609 AGTTTCTATTATAAATTTGGATAAAATTTAATAAATAAGAGTACTACTGAAAGTCTCAG 1668
Db 241 AGTTTCTATTATAAATTTGGATAAAATTTAATAAATAAGAGTACTACTGAAAGTCTCAG 300
QY 1669 ATGACTAATATTATGCTATAGTTAAATGGCTTAAATAATTTAACTGTTAACTTTTTT 1728
Db 301 ATGACTAATATTATGCTATAGTTAAATGGCTTAAATAATTTAACTGTTAACTTTTTT 358
QY 1729 CCACCAAACTCATTATAATATTTTTCATAGGCAAGTTTCTCCTCAG 1774
Db 359 CCA-CAAACTCATTATAATATTTTTCATAGGCAAGTTTCTCCTCAG 403

RESULT 4
US-09-920-300A-1176/c
; Sequence 1176, Application US/09920300A
; Patent No. US30030136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1176
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1176

Query Match 17.5%, Score 310; DB 10; Length 435;
Best Local Similarity 97.4%; Pred. No. 1.7e-70;
Matches 336; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 1430 CTGCTAAACCATGAACCAAAATCTGTGGCAGTGGATGTTATTCCTCATGNGNSAACCC 1489
Db 435 CTGCTAAACCATGAACCAAAATCTGTGGCAGTGGATGTTATTCCTCATGNGNSAACCC 376
QY 1490 ACCTTTCAAGAACACCAAACTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 1549
Db 375 ACCTTTCAAGAACACCAAACTCCTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTAA 316
QY 1550 AATCTGTAAATAGAAAACCTTGAACCATTTAGTATAACAGAACTGCAACTCAGGCGCTA 1609
Db 315 AATCTGTAAATAGAAAACCTTGAACCATTTAGTATAACAGAACTGCAACTCAGGCGCTA 256
QY 1610 GTTCTATTATAAATTTGGATAAAATTTAATAAATAAGAGTACTACTGAAAGTCTCAG 1669
Db 255 GTTCTATTATAAATTTGGATAAAATTTAATAAATAAGAGTACTACTGAAAGTCTCAG 196
QY 1670 TGAATATATTATGCTATAGTTAAATGGCTTAAATAATTTAACTGTTAACTTTTTTTC 1729
Db 195 TGAATATATTATGCTATAGTTAAATGGCTTAAATAATTTAACTGTTAACTTTTTTTC 138
QY 1730 CACCAAACTCATTATAATATTTTTCATAGGCAAGTTTCTCCTCAG 1774
Db 137 CA-CAAACTCATTATAATATTTTTCATAGGCAAGTTTCTCCTCAG 94
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Db 13 CAAGGGCTTCTCTGCGGCAACATCTCGGCGAGCGTAACTGTCGCGGCTTCAACG 74
QY 135 AGCTGGAGCTCC--CAGTCTCACTCCATTCCTTCCCGACCTGGCGCGCACCTGTCAA 192
Db 73 AGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 132
QY 193 GACCAGGCTCTCTCACTAGTAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 252
Db 133 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 192
QY 253 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 312
Db 193 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 252
QY 313 TTCCGAGTCTGCGCATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 372
Db 253 TTCCGAGTCTGCGCATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 312
QY 373 GGGGCGCTGAAGCAGTGTGACCGCGGCTACCTCAACGT-GTCTCTGGCGGCGGTTCCCGCACACGG 431
Db 313 TGGAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 372
QY 432 GA 433
Db 373 GA 374

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## RESULT 8

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US-09-935-390A-1
: Sequence 1, Application US/09935390A
: Patent No. US2002007671A1
: GENERAL INFORMATION:
: APPLICANT: Escobedo, Jaime
: Quianjin, Hu
: Garcia, Pablo
: Williams, Lewis T.
: Kothakota, Srinivas
: TITLE OF INVENTION: Secreted Human Proteins
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Chiron Corporation
: STREET: 4560 Horton Street
: CITY: Emeryville
: STATE: CA
: COUNTRY: USA
: ZIP: 94608-2916
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/935,390A
: FILING DATE: 22-Aug-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/988,671
: FILING DATE: 1997-12-11
: ATTORNEY/AGENT INFORMATION:
: NAME: Jane E. R. Potter
: REGISTRATION NUMBER: 33,332
: REFERENCE/POCKET NUMBER: 1364 002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (510) 923-2718
: TELEFAX: (510) 655-3542
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2063 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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## FEATURE:

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: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-935-390A-1

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Query Match 11.8%; Score 209; DB 10; Length 2063;
Best Local Similarity 54.6%; Pred. No. 4.4e-44;
Matches 507; Conservative 0; Mismatches 410; Indels 12; Gaps 4;

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QY 339 TCGTGGGCTCTAGTTCGCGAGGCACTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 198
Db 180 TCGTGGGCTCTAGTTCGCGAGGCACTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239
QY 359 ACCTCAACGCTGCTCTGCGGCGGCTCCGCGACACGCGGAGTGAACCGTACGCGTGGAG 458
Db 240 CCGT---GGTAAACATCGAGTACGTGACCGCGGAGACCAACCTGACCGGTGGAGCGT 296
QY 459 GCGAGGAGGCGGTGTAGCGGCGAGCACTGCGCGGTGGAGCGCTGTGGGTGGGGTCTCTG 518
Db 297 GCGAGAGTGGCGGCTTGGCGGAGCACTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 356
QY 519 GCGCGGAGGCGCGCGGCGGCGGCTTAAACGCGCTTAACCGCGGTACCGCGGCGACACG 578
Db 357 TCGCGTGGGCGGCGGCGGCGGAGCACTCGAGGCGCTGCGGCGGCGGCGGCGGCGGCGG 416
QY 579 CGGTTTGGGGAAGCACCGGTGCAAGTCTCTTGGTTGGCGCTCATCCCAACGCGGCGGCG 638
Db 417 CCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 473
QY 639 GCACCTTCGCGAGACAGATCCATCTGGCTTATGAGAGATGGGCGGTGCGAGCGGTATCT 698
Db 474 GCACCTTCAGAGCAAGGTGCTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 533
QY 659 TTAACCTCCGCGGCGGCGGCGGCAATGAGGTGATCCCGCTGCTCACCGCGGCGGCGAG 758
Db 534 ACATGAGGAGCGGTACGCGGAAATCATCACTTTGCGCGGCGGCGGCGGCGGCGGCGG 593
QY 759 TTGTTGCAATCATCTGCGCAATCTGAAAGCGCACAAATTTGCAATCTATTCAAGAG 818
Db 594 TAGTGGTCATTATCATTAGCTATCCAAAGGAGAGAGAAATTTGGAGCTGGTCAAAAAG 653
QY 819 GCATACAAGTCACAATGGTCATAGAAGTAGGGAAGAAACATGCGCCCTTGGTGAATCAC- 877
Db 654 GAATTCGAGTAACGATGACCAIAGGGGTTGGCGCGGCGGCGGCGGCGGCGGCGGCGG 713
QY 878 --TATTCAAATTTTTTCTGCTGCTCTTTTATTATTACGGGCGCAACTGTGGGCT 935
Db 714 GTCAGTCTGTGCTGTTTGTGGCCATTGCTTCATCACTGATGATTATCTCGTTAGCCT 773
QY 936 AITTTATCTTTTATCTGCTGCGAAGGCTACGGAATCGAAGCTCAAGAGCTCAAGAGAC 995
Db 774 GGCTAATATTTTACTATATACAGCGTTTCTCTATATATCTGCTCTCAGATTGGAAGTC 833
QY 996 GCGAATTAAGGCGAGTCTTAAAGAAAGCTATTGGAAGGCTTCAACTACGCGACACTGAAC 1055
Db 834 GCCATAGAAA--AGAACTAAGAAAGTTATTGGCCAGCTTCTACTTCTATCTGTAAGC 890
QY 1056 AAGGAGACAGGAAATTTGGCGCTGATGAGATAGTGTGTGTGTCATTTGAATTTGATA 1115
Db 891 ATGGAGAAAGGGAATTCATGCTGATGCTCAAAATTTGCGAGTGTGATTGAAATTTCA 950
QY 1116 AACCAATGATTTGGTAGCATCTTAACGTGCACACCACTATTTCCTAGACATGTGTG 1175
Db 951 AAGTAAGGATATTATTAGAAATTTGCGCATGCGAAGCACTATTTCATAGAAATGATTG 1010
QY 1176 ACCCATGCTCTTAAACACAGAGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1235
Db 1011 ACCCATGCTCTTAAACACAGAGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1070
QY 1236 TGGGAATTTGAGTGGTGTGTTGAAGATGGA 1264
Db 1071 TAGGATATTTGGGAGAGCGCTGGGCGATGTA 1099

```



CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Chiron Corporation  
 STREET: 4560 Horton Street  
 CITY: Emeryville  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94608-2916  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/935,390A  
 FILING DATE: 22-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/988,671  
 FILING DATE: 1997-12-11  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jane E. R. Potter  
 REGISTRATION NUMBER: 33,332  
 REFERENCE/DOCKET NUMBER: 1369,002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 923-2718  
 TELEFAX: (510) 655-3542  
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1322 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-935-390A-16

Query Match 8.4%; Score 149.2; DB 10; Length 1322;  
 Best Local Similarity 56.1%; Pred. No. 8.4e-29;  
 Matches 302; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

QY 720 ATGAGGTCATCCCATCTCTACCGGGTGCAGTACACATTTGTGCAATCATGATCGGCA 779  
 Db 259 AGGAGCAGTTACCATGACTATCCAGGACTGGAGATATATTTGCTGATGATAACAG 318

QY 780 ATCTGAAGGACACAAAATCTGCAATCTATTCAGAGGACATACAAAGTACAAATGGTCA 839  
 Db 319 AATTGAGGGTAAAGATATTTGAGTTATCTGGAGAAACATCTCTGTACAAATGACAA 378

QY 840 TAGAAGTAGGAAACATGCGCCTTGGG---TGAATCACTATTCAAATTTTTCGTTT 896  
 Db 379 TAGCTGTGGAACCTGSAATGCAACGGAAGAACTTCAGCGGTGGCTCTCTAGCTTCGTG 438

QY 897 CTGTGCTCTTTTATTTATACGGGCAACTGTGGCTATTTTATCTTTTATCTGCT 956  
 Db 439 CAATATCTTTTATTTGATGATATTTCTTCAGCATGGCTCATATTTCTACTCATTC 498

QY 957 GAAGGCTACGGAATGCAAGAGCTCAAGAGCAGGAGCAAGTAAAGGAGAGATGCTA 1016  
 Db 499 AAAAGATCAGGTACACAAATGCAGGACAGGAAACAGGCTGCTCGGAGATGAGCCA 558

QY 1017 AAAAGCTATGGAGGCTTCACTAGGCACATGAAACAGGACAGGAAATTTGGCC 1076  
 Db 559 AGAAGGCATCAGTAATTCACACACAGGACATGAAGAGGGGTGACAGGAAATGACG 618

QY 1077 CTGATGGAGATAGTTGTGCTGCTGATTCGATTTGATAAAGCAAAATGATTTGATGCA 1136  
 Db 619 CAGACTTTGATCTGTGCACTCTGATAGAGAGCTATAGCAGAAATGATGTCGTCGAA 678

QY 1137 TCTTAAGCTGCAACATATTTTTCATAAGACATGTTTACGATATGCTGTTTAAACATA 1196  
 Db 679 TCTCCCTGCAAGTATTTTTCACAAATGCTGGTGGATGCTGCTTACTGTAACATT 738

QY 1197 AGACTGCCCATGTGCAAAATGTGACATACCTTAAACATTTGAGAAATGAGAGT 1254

Db 739 GTACTGTCTATGTCGAACCTTAATATATTAAGGCTCTTGGGAATTTGTGCGCAATTT 796

RESULT 12  
 US-09-764-864-485  
 : Sequence 485, Application US/09764864  
 : Patent No. US20020132753A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Rosen et al.  
 : TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 : FILE REFERENCE: PT23  
 : CURRENT APPLICATION NUMBER: US/09/764,864  
 : CURRENT FILING DATE: 2001-01-17  
 : Prior application data removed - consult PALM or file wrapper  
 : NUMBER OF SEQ ID NOS: 1792  
 : SOFTWARE: Patent In Ver. 2.0  
 : SEQ ID NO 485  
 : LENGTH: 619  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : US-09-764-864-485

Query Match 7.5%; Score 132.6; DB 10; Length 619;  
 Best Local Similarity 60.3%; Pred. No. 1.1e-24;  
 Matches 219; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 869 GTGAATCACTATTCAATTTTTTTCGTTTCGTCTGTCCTTTTATTTATTTACGGCGCAACT 928  
 Db 32 GTGAGCGGCACCTTGGTGTGTTGTCCTCATCTCCTTCATTTCTGCTGATGATCATTTCC 91

QY 929 GTGAGCTATTTTATCTTTTATCTCTGGAAGCTACGGAATGCAAGAGCTCAAGCAGG 988  
 Db 92 CTCGATGGCTGCTCTTTTATTACATCCAGAGGTTTCGATATGCAATGCCAGGATAGG 151

QY 989 AAGCAGAGGCAATTAAGGCGAGATGCTAAAAAGCTATTGGAAGGCTTCAACTACGCACA 1048  
 Db 152 AACGAGCGGCTGCGGGATGACGAAAGAGAAAGCCATCAGCAATCCAGATCAGGACC 211

QY 1049 CTGAACAAGGACAGACAGGAAATTTGGCCCTGATGGAGATGTTGCTGTGCTGCTGCA 1108  
 Db 212 ATCAAGAGGGTGACAGGAAACAGAGTCTGATTTTGACAACTGTGCACTTTGTATTGAA 271

QY 1109 TTGTATAAACAATGATTTGGTACGCATCTTAACGTGCAACCATATTTTCCATAGACA 1168  
 Db 272 GGGTACAAGCCCAATGACGTTTCCGCGATCTGCTGCTGCGGATCTTTTCCACAGTCC 331

QY 1169 TGTGTTGACCATGCGCTGTTTAAACACAACTTTGCGGCTATGTAATGTGACATATCT 1228  
 Db 332 TGTGTTGACCCCTGGCTTCTAGACCATCGTACCTGTCCCATGTGCAAGATGAACATCTT 391

QY 1229 AAA 1231  
 Db 392 AAA 394

RESULT 13  
 US-09-864-761-11364  
 : Sequence 11364, Application US/09864761  
 : Patent No. US20020048763A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Penn, Sharon G.  
 : APPLICANT: Panv, David P.  
 : APPLICANT: Hanzel, David K.  
 : APPLICANT: Chen, Wensheng  
 : TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
 : FILE REFERENCE: Aeonica-X-1  
 : CURRENT APPLICATION NUMBER: US/09/864,761  
 : CURRENT FILING DATE: 2001-05-23  
 : PRIOR APPLICATION NUMBER: US 60/180,312  
 : PRIOR FILING DATE: 2000-02-04  
 : PTO/P APPLICATION NUMBER: US 60/207,456





FILE REFERENCE: 37-21(10297)C  
CURRENT APPLICATION NUMBER: US/09/983,965  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: US 09/465,231  
PRIOR FILING DATE: 1999-12-15  
PRIOR APPLICATION NUMBER: US 60/113,678  
PRIOR FILING DATE: 1998-12-17  
NUMBER OF SEQ ID NOS: 5912  
SEQ ID NO 5079  
LENGTH: 435  
TYPE: DNA  
ORGANISM: Bos taurus  
FEATURE:  
OTHER INFORMATION: Clone ID: 31-LIB34-050-Q1-E1-H3  
US-09-983-965-5079

Query Match 6.3%; Score 112.4; DB 10; Length 435;  
Best Local Similarity 86.0%; Pred No 1.4e-19;  
Matches 160; Conservative 0; Mismatches 21; Indels 5; Gaps 3;  
QY 1587 ACAGAACTGCCAATCAGGCGCTAGTTT-CTATTATAAATTGGATAAATTTTAAATAAATA 1645  
DB 1 ACAGAACTGCCAATCAGGCGCTAGTTT-CTATTATAAATTGGATAAATTTTAAATAAATA 60  
QY 1646 AGAGTGATAGTGAAGTGTGATGACTAATATATGCTATAGTTAAATGGCTTAAAA 1705  
DB 61 AGAATGATAGTGAAGTGTGATGACTAATATATGCTATAGTTAAATGGCTTAAAA 118  
QY 1706 ATATTTAAGCTGTAACTTTTTCACCAAACTCATTATAATTTTTCATAGGCAAGTT 1765  
DB 119 ATACTAAAGCTATTAACTTTTTCACCAAACTCATTATAATTTTTCATAGGCAAGTT 176  
QY 1766 TCCTCT 1771  
DB 177 TCCTCT 182

Search completed: October 31, 2002, 11:45:13  
Job time : 128 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002 08:33:05 : Search time 66 seconds  
(without alignments)  
6326.100 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctgagctccacgcgggt atagggaagttttctcttcag 1774

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB seq \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB seq \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB seq \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB seq \*  
5: /cgn2\_6/ptodata/1/ina/PCNHS\_COMB seq \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1 seq \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	147.6	8.3	1253	2	US-08-786-606-6
2	77	4.3	912	2	US-09-090-567-3
3	76.4	4.3	2605	2	US-08-680-345-4
4	73.8	4.2	1378	1	US-08-075-533-20
5	73.8	4.2	1378	2	US-08-948-176-20
6	73.8	4.2	1378	5	PCT-US91-09160-20
7	73.8	4.2	1556	4	US-09-643-937A-3
8	73.8	4.2	1568	4	US-09-043-937A-1
9	73.2	4.1	1543	4	US-09-227-357-25
10	73	4.1	1545	4	US-09-227-357-125
11	73	4.1	1585	4	US-09-183-861-54
12	73	4.1	1585	4	US-09-022-765-64
13	73	4.1	2775	1	US-08-730-771-1
14	73	4.1	2775	4	US-09-060-208-1
15	73	4.1	3089	1	US-08-472-934-5
16	73	4.1	3089	2	US-08-323-460A-5
17	73	4.1	3089	3	US-08-461-146C-5
18	73	4.1	3089	4	US-08-461-145C-5
19	73	4.1	3089	4	US-08-628-829-9
20	73	4.1	3328	4	US-08-960-048-1
21	71.4	4.0	2045	4	US-08-795-088A-1
22	71	4.0	625	4	US-09-288-143-17
23	70.4	4.0	2085	2	US-08-668-128R-7
24	70.4	4.0	2085	2	US-08-905-445-7
25	69.4	3.9	633	4	US-08-818-112-6
26	69.4	3.9	633	4	US-08-818-111-6
27	69.4	3.9	633	4	US-09-056-556-6

28	69.4	3.9	633	4	US-09-072-596-6
29	68.2	3.8	500	4	US-08-818-112-101
30	68.2	3.8	500	4	US-08-818-111-96
31	68.2	3.8	500	4	US-09-056-556-101
32	68.2	3.8	500	4	US-09-072-596-96
33	67.8	3.8	2418	4	US-09-285-379-1
34	66.6	3.8	2327	4	US-09-149-476-107
35	66.2	3.7	3023	4	US-09-308-022-4
36	66	3.7	752	4	US-08-976-259-108
37	66	3.7	849	3	US-08-646-538-14
38	66	3.7	849	4	US-09-503-222-14
39	66	3.7	1924	4	US-09-424-383-5
40	66	3.7	1958	4	US-09-215-231-9
41	66	3.7	2961	4	US-08-446-935-6
42	66	3.7	3699	3	US-08-646-538-6
43	66	3.7	3699	4	US-09-505-222-6
44	66	3.7	3792	2	US-08-992-334-1
45	66	3.7	3792	3	US-08-302-752-1

## ALIGNMENTS

RESULT 1  
US-08-786-606-6  
: Sequence 6, Application US/08786606  
: Patent No. 5861495  
: GENERAL INFORMATION:  
: APPLICANT: Hillman, Jennifer L.  
: APPLICANT: Au-Young, Janice  
: APPLICANT: Guleman, Roger  
: APPLICANT: Goli, Surya K.  
: TITLE OF INVENTION: NOVEL HUMAN ZINC-BINDING  
: NUMBER OF SEQUENCES: 9  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: Incyte Pharmaceuticals, Inc.  
: STREET: 3174 Porter Drive  
: CITY: Palo Alto  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94304  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FastSeq for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US-08/786,606  
: FILING DATE:  
: CLASSIFICATION: 514  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Billings, Lucy RJ  
: REGISTRATION NUMBER: 36,749  
: REFERENCE/INVENT NUMBER: PP-0173 US  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 415-855-0555  
: TELEFAX: 415-845-4166  
: TELEX:  
: INFORMATION FOR SEQ ID NO. 6:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1253 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
US-08-786-606-6

Query Match 8.3% Score 147.6; DB 2: Length 1253;  
Best Local Similarity 55.9% Pred. No. 2.6e-31;  
Matches 301; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

QY 720 ATGAGTCATCCGATGTCACCGGGTGGAGTACATATTGTTGAATCATGATGAGCA 779  
 Db 242 AGAGGCGAGTATGACATGCTACATCCAGGACGATGAGATATTATGCTGCTGATGAAAG 301  
 QY 780 ATGTAAGGACACAAATTTTCAATCTATTAAAGATGACATATAAATGACATGATG 839  
 Db 302 AATTGAGGCTAAGATATTATTTAGTTTATTTGAGAAACATCTCTGTACAAATGACAA 361  
 QY 840 TAGAAGTAGGAAACACATGCGCTTGGG---TGAATCAGATATCAATTTTTTCGTTT 896  
 Db 362 TAGCTGTGTAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTT 421  
 QY 897 CTGTGCTTTTTTTTATTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 955  
 Db 422 CAATATGCTTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTAT 481  
 QY 957 GAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1016  
 Db 482 AGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541  
 QY 1017 AAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1076  
 Db 542 AGAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 601  
 QY 1077 CTGATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1136  
 Db 602 CAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661  
 QY 1137 TTTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1196  
 Db 662 TTTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 721  
 QY 1197 AGATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1254  
 Db 722 GTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779

RESULT 2  
 US-09-090-567-3  
 : Sequence 3, Application US/09090567  
 : Patent No. 5985649  
 : GENERAL INFORMATION:  
 : APPLICANT: Sullivan, Robert  
 : APPLICANT: Brub, Bruno  
 : APPLICANT: Lgar, Christine  
 : APPLICANT: Gaudreault, Christian  
 : TITLE OF INVENTION: Acrosomal Sperm Protein And  
 : TITLE OF INVENTION: Uses Thereof  
 : NUMBER OF SEQUENCES: 5  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Swabey Ogilvy Penault  
 : STREET: 1600 - 1981 McGill College  
 : CITY: Montreal  
 : STATE: QC  
 : COUNTRY: Canada  
 : ZIP: H3A 2Y3  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: Windows  
 : SOFTWARE: FastSeq for Windows Version 2.0b  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/090,567  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER:  
 : FILING DATE:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Murphy, Kevin P  
 : REGISTRATION NUMBER: 26,674  
 : REFERENCE/DOCKET NUMBER: 13045-2"US" PC/DT

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 514-845-7126  
 TELEFAX: 514-288-8389  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 912 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 US-09-090-567-3

Query Match 4.38; Score 77; DB 2; Length 912;  
 Best Local Similarity 94.18; Pred. No. 1.1e-11;

Matches 80; Conservative 0; Mismatches 5; Indels 0, Gaps 0;

QY 1 AGTGGAGGTCACACCGGCTGGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
 Db 7 AGGTCAGGTCACACCGGCTGGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 66  
 QY 61 AATTCGGACGACCGCAGGAGGCTGC 85  
 Db 67 AATTCGGACGACCGCAGGAGGCTGC 91

RESULT 3  
 US-08-680-395-4  
 : Sequence 4, Application US/08680395  
 : Patent No. 5892010  
 : GENERAL INFORMATION:  
 : APPLICANT: Gray, Joe W.  
 : APPLICANT: Collins, Colin  
 : APPLICANT: Hwang, Soo in  
 : APPLICANT: Godfrey, Tony  
 : APPLICANT: Kowbel, David  
 : APPLICANT: Rommens, Johanna  
 : TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their  
 : TITLE OF INVENTION: Uses  
 : NUMBER OF SEQUENCES: 40  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend and Townsend and Crew LLP  
 : STREET: Two Embarcadero Center, Eighth Floor  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94111-3834  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/680,395  
 : FILING DATE: 15-JUL-1996  
 : CLASSIFICATION:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Bastian, Kevin L.  
 : REGISTRATION NUMBER: 34,774  
 : REFERENCE/DOCKET NUMBER: 021070-056890005  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 576-0200  
 : TELEFAX: (415) 576-0300  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2605 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : FEATURE:  
 : NAME/KEY: -





MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0. Version #1.10  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/043,937A  
FILING DATE: 24-Jul-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FW96/01544  
FILING DATE: 03-OCT-1996  
APPLICATION NUMBER: FR 95,11623  
FILING DATE: 03-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1568 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 278..1306  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-043-937A-1

Query Match 4.2%; Score 73.8; DB 4; Length 1568;  
Best Local Similarity 97.4%; Pred. No. 1.1e-10;  
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACCGCGTGGGCGGCTCTAGAACTAGTGGATCCCGGGCGTCGACGG 60  
|||||  
Db 47 AGCTGGAGCTCCACCGCGTGGGCGGCTCTAGAACTAGTGGATCCCGGGCGTCGACGG 105  
QY 61 AATTCGGCAGGACCGCA 77  
|||||  
Db 107 AATTCGGCAGGACCGCA 123

## RESULT 9

US-09-227-357-26  
Sequence 26, Application US-09-227-357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,924  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932

EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 26  
LENGTH: 1543  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (69)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (717)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (899)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-227-357-26

Query Match 4.1%; Score 73.2; DB 4; Length 1543;  
Best Local Similarity 73.8%; Pred. No. 1.7e-10;  
Matches 93; Conservative 0; Mismatches 33; Indels 0; Gaps 0;



```

STATE: Washington
COUNTRY: USA
ZIP: 98104-7042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-183-861-54

```

Query Match 4.18; Score 73; DB 4; Length 1585;

Best Local Similarity	100.0%	Pred. No. 1	95-10;
Matches	73;	Conservative	0;
		Mismatches	0;
		Indels	0;
		Gaps	0;

QY	1	AGCTGGAGTTCATCATGCGGTGGTGGGCGGTCTACAACTACTGCATCCCAAGGCTTGATGAG	60
Dd	3	AGTGGAGTCCACAGCGGTGGTGGGCGGTCTACAACTACTGCATCCCAAGGCTTGATGAG	62
QY	61	AATTCGGCACAGAG 74 	
Dd	63	AATTCGGCACAGAG 75 	

## RESULT 12

```

1  RES-01 12
2  US-09-02-765-54
3  :
4  : Sequence 54, Application US/090422765
5  :
6  : Patent No. 6375955
7  :
8  : GENERAL INFORMATION:
9  :
10 : APPLICANT: Reed, Steven G.
11 :
12 : APPLICANT: Campos-Nieto, Antonio
13 :
14 : APPLICANT: Webb, John R.
15 :
16 : APPLICANT: Dillon, David C.
17 :
18 : APPLICANT: Skeiky, Yasir A W
19 :
20 : TITLE OF INVENTION: LEISHMANIA A
21 :
22 : NUMBER OF SEQUENCES: 87
23 :
24 : CORRESPONDENCE ADDRESS:
25 :
26 : ADDRESSEE: SEED and BERRY LLP
27 :
28 : STREET: 6300 Columbia Center,
29 :
30 : CITY: Seattle
31 :
32 : STATE: Washington
33 :
34 : COUNTRY: USA
35 :
36 : ZIP: 98104-7092
37 :
38 : COMPUTER READABLE FORM:
39 :
40 : MEDIUM TYPE: Floppy disk
41 :
42 : COMPUTER: IBM PC compatible
43 :
44 : OPERATING SYSTEM: PC-DOS/MS-DOS
45 :
46 : SOFTWARE: PatentIn Release #1.0
47 :
48 : CURRENT APPLICATION DATA:
49 :
50 : APPLICATION NUMBER: US/09/022.
51 :
52 : FILING DATE: 12-FEB-1998
53 :
54 : CLASSIFICATION:
55 :
56 : ATTORNEY/AGENT INFORMATION:

```

```

: NAME: MakI, David J.
: REGISTRATION NUMBER: 31,392
: REFERENCE/PROJECT NUMBER: Z10121 42HC3
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO. 54:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1585 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: OS-09-022-765-54

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Query Match	4.18; Score 74!	DR 4; Length 1585;
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Best Local Similarity	100.0%	Pred No. 1	9e-10	Gaps	0
Matches	73	Conservative	0	Mismatches	0
				Indels	0

QY		1	AAGTGGAGGTCACCGCGGTGGCGGCCTCTAGAACTAGTGATCCCGCGGCTGCAGG	60
Dd		3	AGTGGAGTCCACCGCGGTGGCGGCCTCTAGAACTAGTGGATCCCCGGGCTGCAGG	62
QY		61	AATTCGGCACGAG	73
Dd		63	AATTCGGCACGAG	75

RESULT 13

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FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-730-771-1

Query Match 4.1%; Score 73; DB 1; Length 2775;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGGCTGGCGCGCTCTAGAACTACTGATCCCGCGGCTCCGAG 60  
DB 37 AGCTGAGCTCCACCGGCTGGCGCGCTCTAGAACTACTGATCCCGCGGCTCCGAG 60  
QY 61 AATTCGGCAGGAG 73  
DB 97 AATTCGGCAGGAG 109

## RESULT 14

US-09-060-208-1  
Sequence 1, Application US/09060208  
Patent No. 6221629  
GENERAL INFORMATION:

APPLICANT: Marshall, Lisa  
APPLICANT: Roshak, Amy  
TITLE OF INVENTION: THE DNA SEQUENCE OF HUMAN RP-105  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rafter & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: USA  
ZIP: 19482-0980

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,208  
FILING DATE: April 15, 1998  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F.  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: P0380-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2775 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-09-060-208-1

Query Match 4.1%; Score 73; DB 4; Length 2775;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGGCTGGCGCGCTCTAGAACTACTGATCCCGCGGCTCCGAG 60  
DB 37 AGCTGAGCTCCACCGGCTGGCGCGCTCTAGAACTACTGATCCCGCGGCTCCGAG 60

QY 61 AATTCGGCAGGAG 73  
DB 97 AATTCGGCAGGAG 109

## RESULT 15

US-08-472-934-5  
Sequence 5, Application US/08472934  
Patent No. 575346  
GENERAL INFORMATION:

APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL  
RESPONSIVENESS TO EXTERNAL SIGNALS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive and Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,934  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/440,421  
FILING DATE: 15-May-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/354,516  
FILING DATE: 21-FEB-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 5,405,941  
FILING DATE: 15-APR-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/323,460  
FILING DATE: 14-Oct-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11690  
FILING DATE: 14-Oct-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04178  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Giulio A. DeConti, Jr., Esq.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: CPI-004DVCP2  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3089 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 400...2280  
US-08-472-934-5

Query Match 4.1%; Score 73; DB 1; Length 3089;  
Best Local Similarity 100.0%; Pred. No. 2.8e-10;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGAGCTCCACCGGCTGGCGCGCTCTAGAACTACTGATCCCGCGGCTCCGAG 60  
DB 37 AATTCGAGCTCCACCGGCTGGCGCGCTCTAGAACTACTGATCCCGCGGCTCCGAG 60

Db 11 AGCTGGAGCTCCACCGCGGTTGGGAGCTCTAGAACTAGTGGATCCCCCGGGCTGGCAGG 70  
Qy 61 AATTGGGCACGAG 73  
Db 71 AATTGGGCACGAG 83

Search completed: October 31, 2002, 10:33:20  
Job time : 92 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 09:41:15 : Search time 3203 Seconds  
(without alignments)  
16088 619 Million cell updates/sec

Title: US-09-854-300-7  
Perfect score: 1774  
Sequence: 1 agatggagctccacgggtt : aggregated from tag 1774

Scoring table: OLTGO\_NMR  
Gapop 60.0, Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 75 summaries

Database:

GenEmbl:

- 1: gb\_ba:\*
- 2: gb\_hgt:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
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- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
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- 14: gb\_vi:\*
- 15: em\_ba:\*
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- 19: em\_mu:\*
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- 33: em\_hgt\_mus:\*
- 34: em\_hgt\_pln:\*
- 35: em\_hgt\_rod:\*
- 36: em\_hgt\_man:\*
- 37: em\_hgt\_vrt:\*
- 38: em\_sy:\*
- 39: em\_hgt\_hum:\*
- 40: em\_hgt\_mus:\*
- 41: em\_hgt\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1417	79.9	2796	6	AX337968 Sequence
2	1336	75.3	2830	9	AK074264 Homo sapi
3	715	40.3	1297	9	AF394689 Homo sapi
4	625	35.2	169812	9	AL391315 Human DNA
5	625	35.2	169863	2	AL591467 Homo sapi
6	395	22.3	1871	9	AK027169 Homo sapi
7	292	16.5	404	6	AX071980 Sequence
8	275	15.5	646	6	AX341568 Sequence
9	167	9.4	435	6	AX396961 Sequence
10	77	4.3	912	6	AR087649 Sequence
11	76	4.3	1585	8	OSCHINDPR
12	75	4.2	1605	6	AX027925 Sequence
13	74	4.2	851	3	FE286120
14	74	4.2	1190	6	AB4916 Sequence 7
15	74	4.2	1701	6	AB210670 Sequence
16	74	4.2	1701	9	AB028859 Homo sapi
17	74	4.2	1798	8	ATCXC2B
18	74	4.2	2448	4	OCU132110
19	74	4.2	2605	6	AR070327 Sequence
20	73	4.1	518	8	AB005878 Nicotiana
21	73	4.1	545	6	AR184181 Sequence
22	73	4.1	742	6	AX406874 Sequence
23	73	4.1	1365	3	PD0316541
24	73	4.1	1388	6	AX101122 Sequence
25	73	4.1	1556	6	A62300 Sequence 3
26	73	4.1	1556	6	AR145438 Sequence 1
27	73	4.1	1568	6	A62298 Sequence 1
28	73	4.1	1568	6	AR145427 Sequence
29	73	4.1	1585	6	AP202707 Sequence
30	73	4.1	1585	6	AX134055 Sequence
31	73	4.1	1585	6	AX286133 Sequence
32	73	4.1	1724	8	AB075903 Avicennia
33	73	4.1	1731	10	AY012159 Mus muscu
34	73	4.1	2046	8	AF060519 Cuphea ho
35	73	4.1	2186	3	FVA250829
36	73	4.1	2503	6	AX033851 Sequence
37	73	4.1	2775	6	AP018138 Sequence
38	73	4.1	3089	6	AR008278 Sequence
39	73	4.1	3089	6	AR068732 Sequence
40	73	4.1	3089	6	AR085074 Sequence
41	73	4.1	3089	6	AR098267 Sequence
42	73	4.1	3089	6	AR181005 Sequence
43	73	4.1	3328	6	AR164434 Sequence
44	73	4.1	3514	6	AX451794 Sequence
45	73	4.1	4483	9	AF058696 Homo sapi
46	73	4.1	120793	2	AF322450 Homo sapi
47	72	4.1	1711	6	A82595 Sequence 3
48	72	4.1	1711	6	A82786 Sequence 1
49	71	4.0	1179	8	AF315589 Petunia x
50	71	4.0	2045	6	AF156902 Sequence
51	70	3.9	562	3	DMELAST
52	70	3.9	1352	8	THA243514 Trichoder
53	70	3.9	1387	6	AX047063 Sequence
54	70	3.9	1424	6	AX180959 Sequence
55	70	3.9	1460	6	AX047064 Sequence
56	70	3.9	1815	8	AB075902 Avicennia
57	70	3.9	1972	8	AJ269534 Trichoder
58	70	3.9	2085	6	AR060385 Sequence
59	68	3.8	1169	6	AX364844 Sequence
60	68	3.8	2021	5	AB070851 Xenopus l
61	68	3.8	2993	6	AX021518 Sequence
62	68	3.8	3050	4	AF033623 Ovis arie
63	67	3.8	500	6	AR169202 Sequence
64	67	3.8	500	6	AR182492 Sequence
65	67	3.8	500	6	AR194875 Sequence







QY 1174 TGACCCATGGCTGTATTAACACACAGACTTGCCTCCATGTCGCAATGTGACATACATCAAGC 1233  
 Db 922 TGACCATGGCTGTATTAACACACAGACTTGCCTCCATGTCGCAATGTGACATACATCAAGC 951  
 QY 1234 TTGGGAATGAGTGTGATGTTGAAGATGATGATCAGTGTCTTTTAAAGTCCCTGATCCAA 1293  
 Db 982 TTGGGAATGAGTGTGATGTTGAAGATGATGATCAGTGTCTTTTAAAGTCCCTGATCCAA 1041  
 QY 1294 TGAATATCTTAATATGCT 1352  
 Db 1042 TGAATATCTTAATATGCT 1101  
 QY 1354 TGCATATGCTCAGTATGAGACAGATGAGACAGATGAGACAGATGAGACAGATGAGACAG 1413  
 Db 1102 TGCATATGCTCAGTATGAGACAGATGAGACAGATGAGACAGATGAGACAGATGAGACAG 1161  
 QY 1414 AAATCAAAAGTGTATGATGTGTAAATATATGAAGTAAATTTCTGATGATGATGATGATG 1472  
 Db 1162 AAATCAAAAGTGTATGATGTGTAAATATATGAAGTAAATTTCTGATGATGATGATGATG 1221  
 QY 1474 TCATGTCAGACACCCAGCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1533  
 Db 1222 TCATGTCAGACACCCAGCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1281  
 QY 1534 AGAATTAATCTTAA 1549  
 Db 1282 ACAAATTAATCTTAA 1297

RESULT 4  
 AL391315  
 LOCUS Human DNA sequence from clone RP11-150F24 on chromosome X, complete sequence.  
 ACCESSION AL391315  
 VERSION AL391315.22 GI:114575271  
 KEYWORDS HTG  
 SOURCE human  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 169812)  
 Direct Submission  
 Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 requests: clonesrequest@sanger.ac.uk  
 On Jun 28, 2001 this sequence version replaced gi:114575271.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em: EMBL; Sw:  
 SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP  
 database can be found at  
[http://www.sanger.ac.uk/Projects/H\\_sapiens/WormPEP/](http://www.sanger.ac.uk/Projects/H_sapiens/WormPEP/) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome X, constructed by the Sanger Centre Chromosome X Mapping  
 Group. Further information can be found at  
<http://www.sanger.ac.uk/XGP/ChrX>  
 RP11-150F24 is from the library RP11-1.1 constructed by the group  
 of Pieter de Jong. For further details see  
<http://www.sanger.ac.uk/bacterial/chrX/>

## VECTOR: pBAce3.6

This sequence is the entire insert of clone RP11-150F24. The true  
 left end of clone RP11-1.1 is at 8861 in this sequence. The true  
 right end of clone RP11-69763 is at 161410 in this sequence.

## FEATURES

## source

## Location/Qualifiers

1..169812  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="X"  
 /clone="RP11-150F24"  
 /clone\_lib="RP11-1.1"  
 12..569  
 /note="match: GSS: Em:AQ375615"  
 94..165  
 /note="2 copies of 90% conserved"  
 512..729  
 /note="MIR repeat: matches 3..238 of consensus"  
 1338..1638  
 /note="AluY repeat: matches 1..304 of consensus"  
 3599..3642  
 /note="L2 repeat: matches 2707..2750 of consensus"  
 3722..3899  
 /note="MIR repeat: matches 12..171 of consensus"  
 3915..4028  
 /note="MIR repeat: matches 131..238 of consensus"  
 5121..5197  
 /note="L2 repeat: matches 2611..2710 of consensus"  
 6734..7029  
 /note="AluSp repeat: matches 1..297 of consensus"  
 7660..7955  
 /note="AluSq repeat: matches 1..308 of consensus"  
 8891..8940  
 /note="L1F9 repeat: matches 6114..6163 of consensus"  
 10067..10370  
 /note="AluX repeat: matches 1..297 of consensus"  
 10411..10695  
 /note="AluX repeat: matches 1..288 of consensus"  
 10737..10879  
 /note="MER3 repeat: matches 5..154 of consensus"  
 11078..11380  
 /note="AluY repeat: matches 1..300 of consensus"  
 11571..12560  
 /note="LIMD2 repeat: matches 5328..6331 of consensus"  
 13476..13794  
 /note="LIM1 repeat: matches 5417..6165 of consensus"  
 13906..14041  
 /note="L2 repeat: matches 2536..2671 of consensus"  
 14106..14411  
 /note="AluY repeat: matches 2..306 of consensus"  
 16413..16704  
 /note="AluX repeat: matches 1..295 of consensus"  
 17566..17697  
 /note="FLAM\_C repeat: matches 1..132 of consensus"  
 17839..18080  
 /note="MIR repeat: matches 3..260 of consensus"  
 18961..19153  
 /note="MIR repeat: matches 30..262 of consensus"  
 19562..19658  
 /note="MER5A repeat: matches 12..109 of consensus"  
 20326..20413  
 /note="LIMC4 repeat: matches 7861..7948 of consensus"  
 20471..20754  
 /note="AluSq repeat: matches 1..286 of consensus"  
 20755..20782  
 /note="14 copies 2 mer to 89% conserved"  
 20999..21184  
 /note="L2 repeat: matches 2529..2729 of consensus"  
 21194..21952  
 /note="L2 repeat: matches 1730..2546 of consensus"  
 22817..23035  
 /note="MIR repeat: matches 15..238 of consensus"  
 23641..24552  
 /note="cpg island"

## misc\_feature









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Db 121 AACCTTTGAGAGAGCAAACTGCTTAATCAAGAGACTGTTTTCAGAGAAATTAATCTTA 160
QY 1549 AATCTGTGTAATAAGAAAAGTGAACCAATTAGTAATAACAGAACTGCCAATCAGGSCCT 1608
Db 181 AATCTGTGTAATAAGAAAAGTGAACCAATTAGTAATAACAGAACTGCCAATCAGGSCCT 240
QY 1609 AGTTTCTATTATAAATGGATAAATTTAATAAATAGAGTGTATAGTAAAGTGCTAG 1668
Db 241 AGTTTCTATTATAAATGGATAAATTTAATAAATAGAGTGTATAGTAAAGTGCTAG 300
QY 1669 ATGACTAATATATGCTATAGTAA 1694
Db 301 ATGACTAATATATGCTATAGTAA 326

RESULT 9
LOCUS AX396961 435 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1176 from Patent WO0212328.
ACCESSION AX396961
VERSION AX396961.1 GI:21067708
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS King G.E., Meagher M.J., Xu J. and Secriest, H.
TITLE Compositions and methods for the therapy and diagnosis of colon
cancer
JOURNAL Patent: WO 0212328-A 1176 14-FEB-2002.
FEATURES
source
Location/Qualifiers
1..435
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 147 a 62 c 69 g 157 t
ORIGIN
Query Match 9.48; Score 167; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 3.6e-86;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 TTTTCGAGAAATTAATCTTAAATCTGTGTATATAGAACTGACCAATTAATTAATTA 1587
Db 337 TTTTCGAGAAATTAATCTTAAATCTGTGTATATAGAACTGACCAATTAATTAATTA 278
QY 1588 CAGAAATCTGATAGAGGCTAGTCTTATTAATAAATTCATATAAATTAATTAATTAAC 1647
Db 277 CAGAAATCTGATAGAGGCTAGTCTTATTAATAAATTCATATAAATTAATTAATTAAC 218
QY 1648 AGTGATCTGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1694
Db 217 AGTGATCTGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 171

RESULT 10
LOCUS AR087649 912 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from patent US 5989549.
ACCESSION AR087649
VERSION AR087649.1 GI:10014412
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Sullivan P., Berube R., Legare C and Gaudreault C.
TITLE Acrosomal sperm protein and uses thereof
JOURNAL Patent: US 5989549-A 3 24-NOV-1999.
FEATURES
source
Location/Qualifiers
1..912
/organism="unknown"

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BASE COUNT 187 a 279 c 286 g 160 t
ORIGIN
Query Match 4.38; Score 77; DB 6; Length 912;
Best Local Similarity 100.0%; Pred. No. 5.5e-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGACTCCACGGGGGTGGCGGCGCTCTAGAACTAGTATCCCGCGGCTCGAG 60
Db 7 AGCTGAGACTCCACGGGGGTGGCGGCGCTCTAGAACTAGTATCCCGCGGCTCGAG 66
QY 61 AATTCGGCAGCAGCCGA 77
Db 67 AATTCGGCAGCAGCCGA 83

RESULT 11
LOCUS OSCHINDP 1585 bp mpna linear PLN 13-SEP-1995
DEFINITION O.sativa mRNA for chilling-inducible protein.
ACCESSION 254153
VERSION 254153.1 GI:984755
KEYWORDS
SOURCE Oryza sativa (Japonica cultivar-group).
ORGANISM Oryza sativa (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eurhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Binh L.
TITLE Complete sequence of a cDNA related to chilling tolerance in rice
(Oryza sativa L.)
JOURNAL Unpublished
REFERENCE
AUTHORS Binh L. and Oono K.
TITLE Molecular cloning and characterization of genes related to chilling
tolerance in rice
JOURNAL Plant Physiol. 99, 1146-1150 (1992)
REMARK
3 (bases 1 to 1585)
REFERENCE
AUTHORS Binh L.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1995) Binh L., Institute of Biotechnology (IBT),
MST, Plant Cell Biotechnology, Nghiadi, Tuliem, Hanoi, Vietnam,
10000
FEATURES
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Location/Qualifiers
1..1585
/organism="Oryza sativa (Japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="pR601"
/clone_lib="lambda Uni-Zap"
/dev_stage="seedling"
199..1338
/citation=[2]
/citation=[1]
/codon_start=1
/evidence-experimental
/product="chilling-inducible protein"
/protein_id="CAA90866.1"
/db_xref="GI:984756"
/db_xref="SPTREMBL:Q40666"
/translation="MVEVEVSNKQVOMRLHPAAAAEEEDADLPALFDKASHLHS
LASSSDQEGTRKGVLLRRCTDMVSKVGLFSSNETKDDISTANCKLYLVVYDGM
TERVAQEDIPVLKASQCHKEFISICEALELISELEISPKNLIPLWLEHPLH
GSAKPLQKQSSPIPEKPPPPHSSGLSAPIELGDLRLMKEKREGMVSYYLIGS
IEGDLLEMLKKEETIPAVKSGKPMVHLLKLMNVKGLKHGTIMLPTVHTPN
QLIQLSVLVTSEERMAQVFPSEYKLPIMSIEFAGLLEKMKMKKQERTAKMIQESN
SAWHKGSSESAVEDELAEEKAKGKEDWDONPRGAGNKALTPCG"
BASE COUNT 480 a 367 c 418 g 320 t
ORIGIN
Query Match 4.38; Score 76; DB 8; Length 1585;

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 DRAYTRTDVLEMEKIMLSIQFNMSLPTQYLFRLKRLKAGSUKKILILASFLIELAL  
 VOYEWVRPPSLAATAVYTAQCTIHGSEWNSTCEFHCHISENQLLERCFKFWPLHQ  
 KASIDRLTGCVHFKFYSSEFFKATKYIEAHLFVSDSH"

BASE COUNT  
 ORIGIN

553 a 356 c 409 g 480 t

Query Match 4.2%; Score 74; DB 8; Length 1798;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-31;  
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGAGTCCCACTGTCGCGGCTCTAGAACTAGTGGATGATCCCGCGGCTGCAGG 60  
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 Db 82 AGCTGAGTCCCACTGTCGCGGCTCTAGAACTAGTGGATGATCCCGCGGCTGCAGG 141  
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Qy 61 AATTCGGCAGCAGC 74  
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Db 142 AATTCGGCAGCAGC 155  
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RESULT 18  
 LOCUS OCUI32110  
 DEFINITION Oryctolagus cuniculus mRNA for epithelial sodium channel, gamma subunit.  
 ACCESSION AJ132110  
 VERSION 1 GI:4158227  
 KEYWORDS epithelial sodium channel; gamma subunit; gamma-ENaC gene.  
 SOURCE rabbit.  
 ORGANISM Oryctolagus cuniculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 1 (bases 1 to 2448)  
 Kudlacek, O.  
 Direct Submission  
 Submitted (11-JAN-1999) Kudlacek O., Pharmacological Institute,  
 University of Vienna, Waehringerstrasse 13A, A-1090 Wien, AUSTRIA  
 2 (bases 1 to 2448)  
 Kudlacek, O., Weisz, E., Wiener, H. and Plass, H.  
 The rabbit epithelial sodium channel  
 Unpublished  
 Location/Qualifiers  
 source 1..2448  
 /organism="Oryctolagus cuniculus"  
 /db\_xref="taxon:9986"  
 195..2156  
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 195..2156  
 /gene="gamma-ENaC"  
 /codon\_start=1  
 /product="epithelial sodium channel, gamma subunit"  
 /protein\_id="CAA10573.1"  
 /ft\_xref="gi:4158227"

REFERENCE  
 AUTHORS Kudlacek, O., Weisz, E., Wiener, H. and Plass, H.  
 TITLE The rabbit epithelial sodium channel  
 JOURNAL Unpublished  
 FEATURES  
 source 1..2448  
 /organism="Oryctolagus cuniculus"  
 /db\_xref="taxon:9986"  
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 /codon\_start=1  
 /product="epithelial sodium channel, gamma subunit"  
 /protein\_id="CAA10573.1"  
 /ft\_xref="gi:4158227"

BASE COUNT 554 a 778 c 676 g 440 t

Query Match 4.2%; Score 74; DB 4; Length 2448;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-31;  
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGAGTCCCACTGTCGCGGCTCTAGAACTAGTGGATGATCCCGCGGCTGCAGG 60  
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 Db 33 AGCTGAGTCCCACTGTCGCGGCTCTAGAACTAGTGGATGATCCCGCGGCTGCAGG 92  
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 Qy 61 AATTCGGCAGCAGC 74  
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 Db 93 AATTCGGCAGCAGC 106  
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RESULT 19  
 LOCUS AR070327  
 DEFINITION Sequence 4 from patent US 5892010.  
 ACCESSION AR070327  
 VERSION AR070327.1 GI:7221215  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 2605)  
 AUTHORS Gray, T., Collins, C., Hwang, S.-i., Godfrey, T., Kowbel, D. and  
 Rommens, J.  
 TITLE Genes from the 20013 amplicon and their uses  
 JOURNAL Patent, US 5892010-A 4/06-APR-1999;  
 FEATURES  
 Location/Qualifiers  
 source 1..2605  
 /organism="unknown"  
 BASE COUNT 698 a 625 c 550 g 732 t  
 ORIGIN

Query Match 4.2%; Score 74; DB 6; Length 2605;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-31;  
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGAGTCCCACTGTCGCGGCTCTAGAACTAGTGGATGATCCCGCGGCTGCAGG 60  
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 Db 46 AGCTGAGTCCCACTGTCGCGGCTCTAGAACTAGTGGATGATCCCGCGGCTGCAGG 95  
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Qy 61 AATTCGGCAGCAGC 74  
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Db 96 AATTCGGCAGCAGC 109  
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RESULT 20  
 LOCUS AR005878  
 DEFINITION Nicotiana tabacum mRNA for BY215, partial cds.  
 ACCESSION AR005878  
 VERSION AR005878.1 GI:2280517  
 KEYWORDS BY215.  
 SOURCE Nicotiana tabacum (strain: bright yellow 2) cDNA to mRNA.  
 ORGANISM Nicotiana tabacum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 1 (bases 1 to 518)  
 Kojima, H., Hashizume, K., Imanishi, S. and Nakamura, K.  
 Early jasmonate-inducible genes of tobacco cells  
 Unpublished  
 REFERENCE 2 (bases 1 to 518)  
 Imanishi, S.  
 Direct Submission  
 Submitted (17-JUL-1997) Shunryu Imanishi, School of Agriculture,  
 Nagoya University, Laboratory of Biochemistry, Furo-cho, Chikusa,  
 Nagoya 464-01, Japan (E-mail: i45184@nagucc.cc.nagoya-u.ac.jp,  
 Tel: 052-789-4098, Fax: 052-789-4094)  
 Location/Qualifiers  
 source 1..518  
 /organism="Nicotiana tabacum"  
 /strain="bright yellow 2"  
 /db\_xref="taxon:4097"  
 <1..>518  
 /codon\_start=2

BASE COUNT 554 a 778 c 676 g 440 t

Query Match 4.2%; Score 74; DB 4; Length 2448;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-31;  
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Db 1 GCTGGAGTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCA35A 60
QY 62 ATTGGGCACGAGC 74
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Db 61 ATTGGGCACGAGC 73
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RESULT 24
LOCUS AX101122 1388 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 1 from Patent WO0121650.
ACCESSION AX101122
VERSION AX101122.1 GI:13619973
KEYWORDS
SOURCE
ORGANISM
  Dimorphotheca.
  Dimorphotheca
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots;
  Asteridae, euasterids II; Asterales; Asteraceae; Asteroideae;
  Calenduleae.
  1 (bases 1 to 1388)
  Coldren,C., Flint,D., Hallahan,D.L. and Wang,H.
  Cis-prenyltransferases from plants
  Patent: WO 0121650-A 1 29-MAR-2001
  E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES
  source
  1..1388
  /organism="Dimorphotheca"
  /db_xref="taxon:13490"
BASE COUNT 437 a 268 c 297 g 386 t
ORIGIN

Query Match 4 1%; Score 73; DB 6; Length 1388;
Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCTGGAGTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCA35A 61
Db 213 GCTGGAGTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCA35A 272

QY 62 ATTGGGCACGAGC 74
      |||||
Db 273 ATTGGGCACGAGC 285

RESULT 25
LOCUS A62300 1556 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 3 from Patent WO9712982.
ACCESSION A62300
VERSION A62300.1 GI:3716263
KEYWORDS
SOURCE
ORGANISM
  unidentified.
  unidentified
  unclassified.
  1 (bases 1 to 1556)
  Boudet,A., Pichon,M., Grima-Pettenati, Jacqueline, Beckett,M.,
  Gamas,P., Briat and Jean-Francois.
  DNA SEQUENCES CODING FOR A CINNAMOYL COA REDUCTASE, AND
  APPLICATIONS THEREOF IN THE CONTROL OF LIGNIN CONTENTS IN PLANTS
  Patent: WO 9712982-A 3 10-APR-1997
  CENTRE NAT RECH SCIENC (FR)
  other publication FR 2739395 970404
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  195..1310
  /note="unnamed protein product"
  /codon_start=1
  /protein_id="CAA03626.1"
  /db_xref="GI:3716263"
  /translation="MTVVAVVSSSTTAGAFAAAAPVFAAGNGLTVTVTAAYIAWLI"

Query Match 4.1%; Score 73; DB 6; Length 1556;
Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCA35 60
      |||||
Db 52 AGCTGGAGTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCA35 111

QY 61 AATTCGGCAGCAG 73
      |||||
Db 112 AATTCGGCAGCAG 124

RESULT 26
LOCUS ARI45428 1556 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6211432.
ACCESSION ARI45428
VERSION ARI45428.1 GI:15107295
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unknown.
  unclassified.
  1 (bases 1 to 1556)
  Boudet,A., M., Pichon,M., Grima-Pettenati,J., Beckett,M., Gamas,P.
  and Briat,J.-F.
  DNA sequences coding for a cinnamoyl CoA reductase, and
  applications thereof in the control of lignin contents in plants
  Patent: US 6211432-A 3 03-APR-2001
  Location/Qualifiers
  1..1556
  /organism="unknown"
BASE COUNT 304 a 500 c 505 g 247 t
ORIGIN

Query Match 4.1%; Score 73; DB 6; Length 1556;
Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCA35 60
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Db 52 AGCTGGAGTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGCTGCA35 111

QY 61 AATTCGGCAGCAG 73
      |||||
Db 112 AATTCGGCAGCAG 124

RESULT 27
LOCUS A62298 1569 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 1 from Patent WO9712982.
ACCESSION A62298
VERSION A62298.1 GI:3716261
KEYWORDS
SOURCE
ORGANISM
  unidentified.
  unidentified
  unclassified.
  1 (bases 1 to 1568)
  Boudet,A., Pichon,M., Grima-Pettenati, Jacqueline, Beckett,M.,
  Gamas,P., Briat and Jean-Francois.
  DNA SEQUENCES CODING FOR A CINNAMOYL COA REDUCTASE, AND
  APPLICATIONS THEREOF IN THE CONTROL OF LIGNIN CONTENTS IN PLANTS
  Patent: WO 9712982-A 3 10-APR-1997
  Location/Qualifiers
  1..1569
  /organism="unidentified"
  /db_xref="taxon:32644"
  195..1310
  /note="unnamed protein product"
  /codon_start=1
  /protein_id="CAA03626.1"
  /db_xref="GI:3716261"
  /translation="MTVVAVVSSSTTAGAFAAAAPVFAAGNGLTVTVTAAYIAWLI"

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COMMENT CENTRE NAT RECH SCIENT (FR)  
Other publication PP 2739395 970404  
FEATURES Location/Qualifiers  
1..1568  
source

CDS  
278..1306  
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/db\_xref="taxon:32644"  
/organism="unidentified"  
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RGTERRDDPKNGHLKLEGAKEPTLTFVLLILLNSVEAVNGCHGVPHTASPTDN  
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CFKFNMYCYGYAVAAAEAAVAKKEGVLVYVYFVLVLPGLQFTIRASTHILKYL  
TGSAPKTANATQAVVHVRDVALAHILVYKPSAGPYLCAETSLHPRGLVEILAYFP  
EYPIPTKCSREKNPPVPHIFSNKFLKDLQLEPTVPVSECLYEVKSLQCCCHLSIFNK  
EDSLAVKS"

BASE COUNT 478 a 335 c 336 g 419 t  
ORIGIN

Query Match 4.1%; Score 73; DB 6; Length 1568;

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
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Db 47 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 106

QY 61 AATTCGGCAGG 73  
|||||

Db 107 AATTCGGCAGG 119

RESULT 28

ARI45427

LOCUS ARI45427

DEFINITION Sequence 1 from patent US 6211432.

ACCESSION ARI45427

VERSION ARI45427.1 GI:15107294

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1568)

AUTHORS Boudet, A.-M., Pichon, M., Grima-Pettenati, J., Beckert, M., Gamas, P.

and Briat, J.-F.

TITLE DNA sequences coding for a cinnamoyl CoA reductase, and

applications thereof in the control of lignin contents in plants

JOURNAL Patent: US 6211432-A 1 03-APR-2001

FEATURES Location/Qualifiers

1..1568

source

/organism="unknown"

BASE COUNT 479 a 334 c 336 g 419 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
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Db 47 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 106

QY 61 AATTCGGCAGG 73  
|||||

Db 107 AATTCGGCAGG 119

RESULT 29

ARI202707

LOCUS ARI202707

DEFINITION Sequence 54 from patent US 6365165.

ACCESSION ARI202707

VERSION ARI202707.1 GI:15107294

KEYWORDS

SOURCE

ORGANISM

Leishmania major.

Leishmania major

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

ACCESSION ARI202707

VERSION ARI202707.1

LOCUS ARI202707.1

DEFINITION Sequence 54 from Patent WO0179276.

ACCESSION ARI202707

VERSION ARI202707.1

KEYWORDS

SOURCE

ORGANISM

Leishmania major.

Leishmania major

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Leishmania.

REFERENCE 1

AUTHORS

Reed, S.G., Campos-Neto, A., Webb, J.R., Dillon, D.C., and Skeiky, Y.A.W.

TITLE Leishmania antigens for use in the therapy and diagnosis of

Leishmaniasis

JOURNAL Patent: US 6365165-A 54 02-APR-2002;

FEATURES Location/Qualifiers

1..1585

source

/organism="unknown"

BASE COUNT 315 a 567 c 397 g 305 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
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Db 3 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 62

QY 61 AATTCGGCAGG 73  
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Db 63 AATTCGGCAGG 75

RESULT 30

AXI34055

LOCUS AXI34055

DEFINITION Sequence 54 from Patent EP113073.

ACCESSION AXI34055

VERSION AXI34055.1 GI:14270210

KEYWORDS

SOURCE

ORGANISM

unidentified.

Unclassified.

FEATURES Location/Qualifiers

1..1585

source

/organism="unidentified"

/db\_xref="taxon:32644"

BASE COUNT 315 a 567 c 397 g 305 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
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Db 3 AGCTGAGCTCCACGGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 62

QY 61 AATTCGGCAGG 73  
|||||

Db 63 AATTCGGCAGG 75

RESULT 31

AX286133

LOCUS AX286133

DEFINITION Sequence 54 from Patent WO0179276.

ACCESSION AX286133

VERSION AX286133.1 GI:17046028

KEYWORDS

SOURCE

ORGANISM

Leishmania major.

Leishmania major

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Leishmania.

REFERENCE 1

AUTHORS

Reed, S.G., Campos-Neto, A., Webb, J.R., Dillon, D.C., Skeiky, Y.A.W.

TITLE Leishmania antigens for use in the therapy and diagnosis of

Leishmaniasis

JOURNAL Patent: US 6365165-A 54 02-APR-2002;

FEATURES Location/Qualifiers

1..1585

source

/organism="unknown"

BASE COUNT 315 a 567 c 397 g 305 t

ORIGIN

Query Match

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/db_xref:"taxon:8927"	
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222..1565	
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/protein_id="BA094109.1"	
/db_xref="GI:24069018"	
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BASE COUNT	470 a	509 c	503 g	249 t	
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Best Local Similarity	100.0%:	Pred. No. 1.4e-30:			
Matches 73:	Conservative	0:	Mismatches	0:	Indels 0: Gaps 0:
Query	1	AGCTGAGTCTCATACGCGGCTGGGCGGTCTGTAGAACTAGTGTGATCCCGCGGCTGCAGG	60		
Seq	11	AGCTGAGTCTCATACGCGGCTGGGCGGTCTGTAGAACTAGTGTGATCCCGCGGCTGCAGG	70		

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QY 61 AATTCGGCAGGAG 73
|||||
DB 71 AATTCGGCAGGAG 83

RESULT 34
AF060519
DEFINITION
  Cuphea hookeriana 3-ketoacyl-ACP synthase (Kas4) cDNA, complete
  cds.
  2046 bp mRNA linear PLN 28 OCT-1998
ACCESSION
  AF060519
VERSION
  AF060519.1 GI:3800748
KEYWORDS
  Cuphea hookeriana.
SOURCE
  Cuphea hookeriana.
  Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta:
  Spermatophyta: Magnoliopsida: eudicotyledons: Core eudicots;
  Rosidae: eurosids II: Myrtales: Lythraceae: Cuphea.
REFERENCE
  1 (bases 1 to 2046)
  Rehesh, K., Edwards, P., Fillatti, J., Slabaugh, M. and Byrne, J.
  KAS IV: a 3-ketoacyl-ACP synthase from Cuphea sp. is a medium chain
  specific condensing enzyme
  Plant J. 15 (3), 383-390 (1998)
JOURNAL
  MEDLINE
  98422743
PUBMED
  9750349
REFERENCE
  2 (bases 1 to 2046)
  Dehesh, K.
  Direct Submission
  Submitted (20-APR-1998) Gills division, Calgene, 1420 Fifth Street,
  Davis, CA 9561, USA
JOURNAL
  Location/Qualifiers
FEATURES
  source
    1..2046
      /organism="Cuphea hookeriana"
      /db_xref="taxon:36775"
  gene
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      /gene="Kas4"
  CDS
    125..1729
      /gene="Kas4"
      /note="KAS IV"
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      /product="3-ketoacyl-ACP synthase"
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      /db_xref="GI:3800749"
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      DCSQPTPIAGEIKSFSDGVAPKFEPMDFYMLTAGKALADGSGITEDAMKEL
      NKRKGVLIGSLGGMVFVSUSIEALRTSYKKISPFQVPSFTTHMSAILACMDLGMG
      PNYSTACATSNFCILNAAHHIKGEADMLCGGSDAAYLPGVLGDFVACRALSORN
      NQPTKASRPWQSNRDPGFVYMGEGACVLLILELEHAKKPCATLIYAEFLGSGSTCCAYHWT
      EHPFGAGVILICIEKALAGQSVSRFDVNYINAHATSTPAGDINKEYQALAHCPQNSL
      RVNSTKSMIGHILGGAGRAVAVVVAIFGIWHENINLELPEGVLAEFLLVJPKLEY
      LKKVYGLSNFSGFSGHNSIILFAPCN"
BASE COUNT
  526 a 490 c 512 g 518 t
ORIGIN
  1
Query Match
  4.1% Score 73; DB 8; Length 2046;
  Best Local Similarity 100.0%; Pred. No. 1.4e-30;
  Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACCGGCTGGGCGCTCTTASAACTAGTGGATGCGCGCGGCGAGG 50
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DB 16 AGCTGGAGTTCACCGGCTGGGCGCTCTTASAACTAGTGGATGCGCGCGGCGAGG 50

QY 61 AATTCGGCAGGAG 73
|||||
DB 76 AATTCGGCAGGAG 88

RESULT 35
PVA250829
LOCUS
  PVA250829
  2186 bp mRNA linear INV 04-APR-2000
  1
Query Match
  4.1% Score 73; DB 3; Length 2186;
  Best Local Similarity 100.0%; Pred. No. 1.4e-30;
  Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACCGGCTGGGCGCTCTTASAACTAGTGGATGCGCGCGGCGAGG 60
|||||
DB 27 AGCTGGAGTTCACCGGCTGGGCGCTCTTASAACTAGTGGATGCGCGCGGCGAGG 60

QY 61 AATTCGGCAGGAG 73
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DB 87 AATTCGGCAGGAG 99

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DEFINITION
  Penaeus vannamei mRNA for phosphoenolpyruvate carboxykinase (pepck
  gene).
ACCESSION
  AJ250829
VERSION
  AJ250829.1 GI:7414465
KEYWORDS
  pepck gene; phosphoenolpyruvate carboxykinase.
SOURCE
  Litopenaeus vannamei.
ORGANISM
  Litopenaeus vannamei.
  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
  Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
  Penaeidae; Litopenaeus.
REFERENCE
  1 (bases 1 to 2186)
  Van Wormhoudt, A.E. and Arena Ortiz, M.L.
  Characterization of phosphoenolpyruvate carboxykinase from Penaeus
  vannamei (Crustacea Decapoda)
  Unpublished
JOURNAL
  Location/Qualifiers
REFERENCE
  2 (bases 1 to 2186)
  Van Wormhoudt, A.E.
  Direct Submission
  Submitted (02-NOV-1999) Van Wormhoudt A.E., Museum National
  d'Histoire Naturelle, CNRS, BP 270, 29900 Concarneau, FRANCE
JOURNAL
  Location/Qualifiers
FEATURES
  source
    1..2186
      /organism="Litopenaeus vannamei"
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      /dev_stage="adult"
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      /gene="pepck"
      /protein_id="Pvpepck"
      /EC_number="4.1.1.32"
      /function="gluconeogenesis"
      /codon_start=1
      /evidence=experimental
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      /protein_id="Pvpepck"
      /db_xref="GI:7414466"
      /translation="MLFLRLNGVLGEARVAEANKLNLAFAARSLATHGSLSLDK
      PKVRSFVEEGARLQCPKNVHICDSERELRLDLNVMQVGMIEPLKRYTNCWLRTDP
      GDVAPVESKFTIVTKDPEITPTKKEGIFGLGNMSPEDLKAVKEPFGCKMGRMT
      YVVPFSGVPGSLKIGIQLTDSYVVASMTMTMKGKAVLDALAEODFVKCLHSVG
      CPLPLQTLVNNPCDPERTIVTHVPTSETISFGSGYGGNTLLGKKKSLPQSTIAL
      REDLAEHLIILGITNPGQVKKYIAALPSACGCTNLAMMTPLPYKKVCEVGDIDIAW
      IKFDGGLRLAINTENPGFVAPGTSMTNPNVAMQTVLSNTIFTNVAKTSDGGVFNEG
      LEKETANDVTITISWLDGNTNSKSGKPAAHPSNLSFCTPAGOSPTIDPAWEDPKGVPTIS
      AILFGRPEGVPLIYFAFSWKGVLVGGAMRSATAAAGKAKVIMHDFAMRPFPG
      YNFGYLGHLMSMTTRTHKALPKIFVHWNFKDEKARFIWPGFGENDRVLDWILRRVD
      GDVAAETIRLLPKPSSLNMGLEDQNLDMHELFLPKPGFWQJETAIAKYFEEVJVG
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BASE COUNT
  510 a 668 c 605 g 403 t
ORIGIN
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Query Match
  4.1% Score 73; DB 3; Length 2186;
  Best Local Similarity 100.0%; Pred. No. 1.4e-30;
  Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCACCGGCTGGGCGCTCTTASAACTAGTGGATGCGCGCGGCGAGG 60
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DB 27 AGCTGGAGTTCACCGGCTGGGCGCTCTTASAACTAGTGGATGCGCGCGGCGAGG 60

QY 61 AATTCGGCAGGAG 73
|||||
DB 87 AATTCGGCAGGAG 99

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RESULT 36  
AX033851  
LOCUS AX033851 2503 bp DNA linear PAT 21-SEP-2000  
DEFINITION Sequence 1 from Patent NO944851.  
ACCESSION AX033851  
VERSION AX033851.1 GI:10280444  
KEYWORDS  
SOURCE Neocallimastix patriciarum.  
ORGANISM Neocallimastix patriciarum.  
Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;  
Neocallimastixaceae; Neocallimastix.  
REFERENCE 1 (bases 1 to 2503)  
AUTHORS Xu, G. P.  
JOURNAL Patent: NO 944851-A 14-FEB-1995;  
COMM. SCIENT. IND. RES. ORG. (AU)  
FEATURES  
source  
1..2503  
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/db\_xref="taxon:4758"  
BASE COUNT 893 a 389 c 517 g 704 t  
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Query Match 4.1%; Score 73; DB 6; Length 2503;  
Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
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DB 52 AGCTGGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGCATCCCGGGTGGGAGG 111  
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QY 61 AATTCGGCAGGAG 73  
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DB 112 AATTCGGCAGGAG 124  
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RESULT 37  
AR081838  
LOCUS AR081838 2775 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 1 from patent US 5780609  
ACCESSION AR081838  
VERSION AR081838.1 GI:3973741  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2775)  
AUTHORS Marshall, L.A. and Poshak, A.K.  
TITLE DNA sequence of human RP-105  
JOURNAL Patent: US 5780609-A 14-JUL-1998;  
FEATURES  
source  
1..2775  
/organism="unknown"  
BASE COUNT 792 a 534 c 545 g 724 t  
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Query Match 4.1%; Score 73; DB 6; Length 2775;  
Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AGCTGGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGCATCCCGGGTGGGAGG 60  
|||||  
DB 37 AGCTGGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGCATCCCGGGTGGGAGG 96  
|||||  
  
QY 61 AATTCGGCAGGAG 73  
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DB 97 AATTCGGCAGGAG 109  
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RESULT 38  
AP008278  
LOCUS AP008278 3089 bp DNA linear PAT 04-SEP-1999  
DEFINITION Sequence 5 from patent US 5753446.

ACCESSION AP008278 1 GI:3967387  
VERSION AP008278.1  
KEYWORDS Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3089)  
AUTHORS Johnson, G.L.  
TITLE Mitogen ERK kinase kinase (MEKK) assay  
JOURNAL Patent: US 5753446-A 5-19-MAY-1998;  
FEATURES  
Location/Qualifiers  
1..3089  
/organism="unknown"  
BASE COUNT 752 a 839 c 871 g 627 t  
ORIGIN  
  
Query Match 4.1%; Score 73; DB 6; Length 3089;  
Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AGCTGGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGCATCCCGGGTGGGAGG 60  
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DB 11 AGCTGGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGCATCCCGGGTGGGAGG 70  
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QY 61 AATTCGGCAGGAG 73  
|||||  
DB 71 AATTCGGCAGGAG 83  
|||||  
  
RESULT 39  
AR068732  
LOCUS AR068732 3089 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5854043.  
ACCESSION AR068732  
VERSION AR068732.1 GI:6000939  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3089)  
AUTHORS Johnson, G.L.  
TITLE MEKK-related signal transduction kinases  
JOURNAL Patent: US 5854043-A 5-29-DEC-1998;  
FEATURES  
Location/Qualifiers  
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BASE COUNT 752 a 839 c 871 g 627 t  
ORIGIN  
  
Query Match 4.1%; Score 73; DB 6; Length 3089;  
Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AGCTGGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGCATCCCGGGTGGGAGG 60  
|||||  
DB 11 AGCTGGAGCTCCACCGGGTGGGGGCTCTAGAACTAGTGCATCCCGGGTGGGAGG 70  
|||||  
  
QY 61 AATTCGGCAGGAG 73  
|||||  
DB 71 AATTCGGCAGGAG 83  
|||||  
  
RESULT 40  
AR085074  
LOCUS AR085074 3089 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 5 from patent US 5981265.  
ACCESSION AR085074  
VERSION AR085074.1 GI:10011845  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3089)

AUTHORS Johnson,G.L.  
TITLE Methods for regulating MEKK protein activity  
JOURNAL Patent: US 5981265-A 5 09-NOV-1999;  
FEATURES Location/Qualifiers  
source  
1..3089  
/organism="unknown"

BASE COUNT 752 a 839 c 871 g 627 t  
ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3089.

Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
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QY 1 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 60  
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Db 11 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 70  
|||||

QY 61 AATTCGGCAGGAG 73  
|||||

Db 71 AATTCGGCAGGAG 83  
|||||

RESULT 41

LOCUS AR098267 3089 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 5 from patent US 6074861.  
ACCESSION AR098267  
VERSION AR098267.1 GI:12807524  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3089)  
AUTHORS Johnson,G.L.  
TITLE MEKK proteins  
JOURNAL Patent: US 6074861-A 5 13-MAY-2000;  
FEATURES Location/Qualifiers  
source  
1..3089  
/organism="unknown"

BASE COUNT 752 a 839 c 871 g 627 t  
ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3089.

Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
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QY 1 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 60  
|||||  
Db 11 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 70  
|||||

QY 61 AATTCGGCAGGAG 73  
|||||

Db 71 AATTCGGCAGGAG 83  
|||||

RESULT 42

LOCUS AP181005 3089 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 9 from patent US 6333170.  
ACCESSION AP181005  
VERSION AP181005.1 GI:20223038  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3089)  
AUTHORS Johnson,G.L.  
TITLE Method and product for regulating cell responsiveness to external  
signals  
JOURNAL Patent: US 6333170-A 9 25-DEC-2001;  
FEATURES Location/Qualifiers  
source  
1..3089  
/organism="unknown"

BASE COUNT 1234 a 723 c 867 g 589 t  
ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3089.  
Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 60  
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Db 11 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 70  
|||||

QY 61 AATTCGGCAGGAG 73  
|||||

Db 71 AATTCGGCAGGAG 83  
|||||

BASE COUNT 752 a 839 c 871 g 627 t  
ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3089.

Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 60  
|||||  
Db 11 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 70  
|||||

QY 61 AATTCGGCAGGAG 73  
|||||

Db 71 AATTCGGCAGGAG 83  
|||||

RESULT 43

LOCUS AR164434 3328 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 1 from patent US 6271443.  
ACCESSION AR164434  
VERSION AR164434.1 GI:16235654  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3328)  
AUTHORS Stalker,D.M., Pear,J.P. and Delmer,D.  
TITLE Cotton and rice cellulose synthase DNA sequences  
JOURNAL Patent: US 6271443-A 1 07-AUG-2001;  
FEATURES Location/Qualifiers  
source  
1..3328  
/organism="unknown"

BASE COUNT 914 a 689 c 763 g 962 t  
ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3328.

Best Local Similarity 100.0%; Pred. No. 1.5e-30;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 60  
|||||  
Db 30 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 89  
|||||

QY 61 AATTCGGCAGGAG 73  
|||||

Db 90 AATTCGGCAGGAG 102  
|||||

RESULT 44

LOCUS AX451799 3513 bp DNA linear PAT 03-JUL-2002  
DEFINITION Sequence 7 from Patent WO0238803.  
ACCESSION AX451799  
VERSION AX451799.1 GI:21698666  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Eichmueller,S., Schadendorf,D. and Usener,D.  
TITLE Novel marker for the diagnosis and therapy of tumours  
JOURNAL Patent: WO 0238803-A 7 16-MAY-2002;  
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OEFFENTLICHEN RECHTS  
(DE)

BASE COUNT 1234 a 723 c 867 g 589 t  
ORIGIN

Query Match 4.1% Score 73; DB 6; Length 3513.  
Best Local Similarity 100.0%; Pred. No. 1.4e-30;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 60  
|||||  
Db 30 AGCTGGAGCTTCAACCGGCGGCTGCTTAGAACTAGTGGATCCGCGCGGCGGCTGCAGG 89  
|||||

QY 61 AATTCGGCAGGAG 73  
|||||

Db 90 AATTCGGCAGGAG 102  
|||||

RESULT 44

LOCUS AX451799 3513 bp DNA linear PAT 03-JUL-2002  
DEFINITION Sequence 7 from Patent WO0238803.  
ACCESSION AX451799  
VERSION AX451799.1 GI:21698666  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Eichmueller,S., Schadendorf,D. and Usener,D.  
TITLE Novel marker for the diagnosis and therapy of tumours  
JOURNAL Patent: WO 0238803-A 7 16-MAY-2002;  
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OEFFENTLICHEN RECHTS  
(DE)



```

* 12275 16059: contig of 3785 bp in length
* gap of unknown length
* 16060 13969: contig of 3910 bp in length
* gap of unknown length
* 19970 22905: contig of 2936 bp in length
* gap of unknown length
* 22906 29210: contig of 4305 bp in length
* gap of unknown length
* 28211 34020: contig of 5810 bp in length
* gap of unknown length
* 34021 41704: contig of 7684 bp in length
* gap of unknown length
* 41705 48302: contig of 6598 bp in length
* gap of unknown length
* 48303 56789: contig of 8487 bp in length
* gap of unknown length
* 56790 65997: contig of 4207 bp in length
* gap of unknown length
* 65997 74434: contig of 8438 bp in length
* gap of unknown length
* 74435 83698: contig of 9264 bp in length
* gap of unknown length
* 83699 95956: contig of 12258 bp in length
* gap of unknown length
* 95957 107954: contig of 11997 bp in length
* gap of unknown length
* 107954 120793: contig of 12840 bp in length
* Location/Qualifiers
  source          1..120793
    organism="Homo sapiens"
    db_xref="taxon:9606"
    chromosome="17"
    map="51p13.3"
    clone="BAC407121"

```

```

BASE COUNT      28674 a 31051 c 31727 g 29285 t      50 others
ORIGIN

```

```

Query Match      4.1%; Score 73; DB 2; Length 12073;
Best Local Similarity 100.0%; Pred. No. 2.1e-30;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ACTGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 60
|||||
DB 9236 ACTGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 60
|||||

```

```

QY 61 AATTGGCAGCAGG 73
|||||

```

```

DB 9296 AATTGGCAGCAGG 9308
|||||

```

```

RESULT 47
A82595      1711 bp      DNA      circular PAT 21-JAN-2000
LOCUS      A82595
DEFINITION Sequence 3 from Patent WO9854316.
ACCESSION  A82595
VERSION    A82595 1 GI:6732340
KEYWORDS
SOURCE     human.

```

```

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates, Catarrhini, Homiidae; Homo.
REFERENCE  1 (bases 1 to 1711)
AUTHORS   Graham D. and Renard S.
TITLE     SODIUM CHANNEL RECEPTOR
JOURNAL   WO 9854316-A 3 03-DEC-1998;
PATENT: WO 9854316-A 3 03-DEC-1998;
          GRAHAM DAVID (FP); RENARD STEPHANE (FP)

```

```

FEATURES
    source          1..1711
      organism="Homo sapiens"
      db_xref="taxon:9606"
      tissue_type="CEREBELLUM"

```

```

BASE COUNT      329 a      578 c      481 g      323 t
ORIGIN

```

```

Query Match      4.1%; Score 72; DB 6; Length 1711;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 CTGGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 62
|||||
DB 1 CTGGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 60
|||||

```

```

QY 63 TTGGCAGCAGG 74
|||||
DB 61 TTGGCAGCAGG 72
|||||

```

```

RESULT 49

```

```

Query Match      4.1%; Score 72; DB 6; Length 1711;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 CTGGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 62
|||||
DB 1 CTGGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 60
|||||

```

```

QY 63 TTGGCAGCAGG 74
|||||
DB 61 TTGGCAGCAGG 72
|||||

```

```

RESULT 48

```

```

A82786      1711 bp      DNA      circular PAT 21-JAN-2000
LOCUS      A82786
DEFINITION Sequence 1 from Patent EP0884386.
ACCESSION  A82786
VERSION    A82786.1 GI:6732465
KEYWORDS
SOURCE     human.

```

```

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 1711)
AUTHORS   Graham D. and Renard S.
TITLE     Sodium channel receptor
JOURNAL   Patent: EP 0884386-A 1 16-DEC-1998;
          SYNTHELABO (FP)

```

```

FEATURES
    source          1..1711
      organism="Homo sapiens"
      db_xref="taxon:9606"
      clone="SLNAC1"
      tissue_type="CEREBELLUM"

```

```

CDS
    76..1632
      /function="SODIUM CHANNEL RECEPTOR"
      /standard_name="SLNAC1"
      /codon_start=1
      /product="SLNAC1"
      /protein_id="CAKK9252.1"
      /db_xref="GI:6732466"

```

```

TRANSLATION="MHGLGHVFGPGSLIPGCMWAAAVLVATFLYQVAVRVRVYRE
FHHQALGERSHRLIPFAVLICNINFLERSRLTNELHAGSALLGLDPAHAAFLR
ALGRPPAPPMPSPPTFDMAQLYAPAGSLDDMLDLCFRPGQCPENFTTIFPMGR
CYTFNSGADGAELLTTFGMGNGLDIMLVQEEYLPVWKNFETPEVGIHVHGS
QREPFILDLGLGVSPGYTFVSCUQQQLSLFPPWDCSSALNPTEPEPDPDLS
PSPSPPYTLMGCRACETRYVAKCGRMVYMPGDVFCVSPQYKNCAPDAIDL
RKDSCACNPACSTRYAKELSMVRIPSRAAAFLLARKLNRSFVIAENVLALDIFEA
LNYETVEQKKAYEMSELLDGGOMGLFAGSLLLILEILYLCVFRKVLGYFVNR
QMSQRHSNLTSHPSLGRHQSLSLPPHLLPCHTALDLSVSSEPRPDILDMPSLHV
AFPSPPQIKS"

```

```

mat_peptide      76..1629
                  /product="H_SLNAC1"
                  /function="Sodium CHANNEL RECEPTOR"
BASE COUNT      329 a      578 c      481 g      323 t
ORIGIN

```

```

Query Match      4.1%; Score 72; DB 6; Length 1711;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 CTGGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 62
|||||
DB 1 CTGGAGCTCCACGCGGCGGCTGAGTAACTAGTGGATCCCGGGGTGCAGGAA 60
|||||

```

```

QY 63 TTGGCAGCAGG 74
|||||
DB 61 TTGGCAGCAGG 72
|||||

```

```

RESULT 49

```

```

AF315589
LOCUS       AF315589                1179 bp    DNA    linear    PLN 01-APR-2001
DEFINITION Petunia x hybrida cv. Dazzler CDC48 cell division-like protein
ACCESSION   AF315589
VERSION     AF315589.1  GI:13492048
KEYWORDS    Petunia x hybrida.
SOURCE      Petunia x hybrida.
ORGANISM   Petunia x hybrida
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Petunia
            1. (bases 1 to 1179)
REFERENCE   Adisheshaiah,P.P. and Kumar,P.P.
AUTHORS     Adisheshaiah,P.P. and Kumar,P.P.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2000) Biological Sciences, National University of
            Singapore, 10 Science Drive 4 117543, Singapore
FEATURES             Location/Qualifiers
     source          1..1179
                     /organism="Petunia x hybrida"
                     /cultivar="Dazzler"
                     /db_xref="taxon:4102"
                     /tissue_type="leaf"
     misc_feature    <1..1011
                     /note="similar to CDC48 cell division protein"
BASE COUNT  341 a 229 c 297 g 312 t
ORIGIN

Query Match      4.0%; Score 71; DB 8; Length 1179;
Best Local Similarity 100.0%; Pred. No. 2e-29;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  ACTTCAAGTCTACAGCGGCTGGGCGGCTGTAGAACTAGTGGATCCCGCGGCTGGAGG 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB  24  AATTCGGACGACG 94
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY  61  AATTCGGACG 71
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB  84  AATTCGGACG 94
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 50
ARI56902
LOCUS       ARI56902                2045 bp    DNA    linear    PAI 08-AUG-2001
DEFINITION Sequence 1 from patent US 6242569.
ACCESSION   ARI56902
VERSION     ARI56902.1  GI:15125606
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 2045)
AUTHORS     Shu,H.-B. and Goeddel,D.V.
TITLE       Regulators of apoptosis
JOURNAL     Patent: US 6242569-A 1 05-JUN-2001;
            Location/Qualifiers
FEATURES             Location/Qualifiers
     source          1..2045
                     /organism="unknown"
BASE COUNT  551 a 475 c 560 g 459 t
ORIGIN

Query Match      4.0%; Score 71; DB 6; Length 2045;
Best Local Similarity 100.0%; Pred. No. 2.1e-29;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3  CTGAGGCTTCCCGCGGCGGCGGCTGTAGAACTAGTGGATCCCGCGGCTGGAGGAA 62
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB  10  CTGAGGCTTCCCGCGGCGGCGGCTGTAGAACTAGTGGATCCCGCGGCTGGAGGAA 69

```

QY 63 TTCGGACGACG 73  
 Db 70 TTCGGACGACG 80

Search completed: October 31, 2002, 11:13:04  
 Job time : 3395 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 10:08:50 ; Search time 1991 Seconds  
(without alignments)  
14430.333 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctggagctccaccaggt..... atagggaagtttctctctcag 1774

Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthba:\*

3: em\_estln:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_Other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	ID	Description
1	591	33.3	1954 11	BC030951 Homo sapi
2	491	27.7	557 13	BM597037 Homo sapi
3	484	27.3	1806 11	BC012931 Homo sapi
4	446	25.1	876 10	AV840700 AV840700
5	446	25.1	683 10	AV886169 AV886169
6	418	23.6	902 12	B3155006 B3155006

7	409	23.1	841	12	BF696359
8	409	23.1	847	12	BE958515
9	395	22.3	683	10	AV692456
10	388	21.9	774	12	BG432146
11	384	21.6	841	12	BF666880
12	376	21.2	811	13	BE600046
13	374	21.1	856	12	BE958087
14	359	20.2	884	12	BF542034
15	349	19.7	879	12	BF666897
16	349	19.7	1000	13	BE600419
17	343	19.3	862	12	BF700761
18	340	19.2	906	12	BG165370
19	329	18.5	773	13	BE601096
20	322	18.2	759	12	BE958295
21	300	16.9	863	12	BF697105
22	298	16.8	872	12	BF699229
23	295	16.6	466	12	BF382058
24	294	16.6	759	12	BG400279
25	287	16.2	482	13	BE715115
26	280	15.8	835	12	BE958350
27	256	14.4	458	14	H48650
28	240	13.5	862	12	BF668554
29	238	13.4	818	12	BF698503
30	228	12.9	854	12	BF670202
31	227	12.8	545	13	BE964160
32	224	12.6	358	14	T50929
33	223	12.6	619	13	BG991456
34	221	12.5	732	12	BF246687
35	220	12.4	400	14	D60241
36	220	12.4	876	12	BF665797
37	214	12.1	807	12	BF701837
38	214	12.1	938	12	BF698234
39	193	10.9	1150	13	BE488609
40	187	10.5	513	12	BE959288
41	186	10.5	693	12	BF696365
42	179	10.1	462	10	AE583705
43	176	9.9	368	14	R24902
44	163	9.2	561	12	BE958612
45	163	9.2	855	12	BF666952
46	161	9.1	234	14	CI5261
47	158	8.9	904	12	BF664617
48	150	8.5	445	10	BE536963
49	145	8.2	769	12	BF032034
50	135	7.6	304	13	BG960989
51	130	7.3	896	12	BF665003
52	127	7.2	562	12	BF131792
53	125	7.0	942	12	BF967109
54	122	6.9	789	12	BF669635
55	108	6.1	718	12	BF029934
56	106	6.0	534	12	BF695871
57	104	5.9	784	12	BF700216
58	96	5.4	160	9	AA155685
59	94	5.3	227	14	DB1750
60	87	4.9	239	14	BQ352573
61	83	4.7	635	12	BF698021
62	83	4.7	676	12	BF697847
63	83	4.7	770	12	BF700926
64	82	4.6	244	14	CI5568
65	80	4.5	1067	13	BM460110
66	79	4.5	801	10	BE421538
67	79	4.5	846	12	BF695972
68	78	4.4	575	10	AW914131
69	77	4.3	149	10	AW914243
70	77	4.3	202	10	AW914219
71	77	4.3	525	14	BQ078956
72	77	4.3	533	14	BQ078956
73	77	4.3	535	10	AW914117
74	77	4.3	652	10	AW913953
75	77	4.3	884	10	BE414171

ALIGNMENTS

## RESULT 1

BC030951  
LOCUS BC030951 1954 bp mRNA linear HTC 13-JUN-2002  
DEFINITION Homo sapiens, hypothetical protein: FLJ23516, clone IMAGE:4280352,  
mRNA.  
ACCESSION BC030951  
VERSION B010451.1 GI:21410659  
KEYWORDS HTC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1954),  
Straussberg, R.  
Direct Submission  
Submitted (03-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-ref@mail.nih.gov](mailto:cgaps-ref@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcdepaxil@stanford.edu](mailto:mcdepaxil@stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

REMARK  
COMMENT

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at <http://img-101.g-w>  
Series: IRAL Plate: 41 Row: C Column: 10  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 13375696  
This clone has the following problem: frame shifted.

## FEATURES

source  
1..1954  
/organism="Homo sapiens"  
/db\_xref="LocusID:79589"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4280352"  
/tissue\_type="Brain, primitive neuroectodermal"  
/clone\_lib="NIH\_MGC\_56"  
/lab\_host="DH10B"  
/note="Vector: pDNR-LIB"  
BASE COUNT 676 a 294 c 346 g 638 t  
ORIGIN

Query Match 33.3% Score 591; DB 11; Length 1954;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 791; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 900 TGTCTTTTATTATTAGSGGGGAATGSGGTATTTATCTTTTATCTCTCAAA 659  
|||||  
Db 1 TGTCTTTTATTATTAGSGGGGAATGSGGTATTTATCTTTTATCTCTCAAA 60  
|||||  
QY 960 GGTCTAGGATGTAAGAGTCAAGAGCAGGAGCAGGCAATTAAGGCGAGATGCTAAAA 1019  
|||||  
Db 61 GGCTACGGAATGCAAGAGCTCAAGCAGGAGCAGGCAATTAAGGCGAGATGCTAAAA 120  
|||||  
QY 1020 AAGCTATTGAAAGTTTCAACTAGCAGTACTGAAACAGAGAGAGTAAGGAAATGAGGCTG 1079  
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Db 121 AAGCTATTGAAAGTTTCAACTAGCAGTACTGAAACAGAGAGAGTAAGGAAATGAGGCTG 180  
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QY 1080 ATGAGATAGCTGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139  
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Db 181 ATGAGATAGCTGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
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QY 1140 TAAAGTGAATATATTTTTCATAGATATGTTGTTTGAATGTTTGAATGTTTGAATGTTTGA 1199  
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Db 241 TAACTGTGAACCATATTTTCCATAGACATGTGTGGCCCATGCTTTAGACACAGGA 300  
|||||  
QY 1200 CTTGCCCATCTGCAAAATGTGCATACATCAAAAGCTTTGGGAATTCAGGTGGATGTTGAAG 1259  
|||||  
Db 301 CTTGCCCATCTGCAAAATGTGCATACATCAAAAGCTTTGGGAATTCAGGTGGATGTTGAAG 360  
|||||  
QY 1250 ATGATACAGTGTCTTTACAAAGTCCCTGTATCAATGAATATTAATAGTCCCTCCCTCC 1319  
|||||  
Db 361 ATGATACAGTGTCTTTACAAAGTCCCTGTATCAATGAATATTAATAGTCCCTCCCTCC 420  
|||||  
QY 1320 ATGAAGAGAGAAATGSCAG 1379  
|||||  
Db 421 ATGAAGAGAGAGAAATGSCAG 480  
|||||  
QY 1380 ATGAAG 1439  
|||||  
Db 481 ATGAAG 540  
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QY 1440 ATGAAG 1499  
|||||  
Db 541 ATGAAG 600  
|||||  
QY 1500 AAG 1559  
|||||  
Db 601 AAG 660  
|||||  
QY 1560 AATAG 1619  
|||||  
Db 661 AATAG 720  
|||||  
QY 1620 ATAAATGGATAAATTTTAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679  
|||||  
Db 721 ATAAATGGATAAATTTTAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
|||||  
QY 1680 TATGCTATAGTATAA 1694  
|||||  
Db 781 TATGCTATAGTATAA 795  
|||||

RESULT 2  
BM507037 557 bp mRNA linear EST 15-FEB-2002  
LOCUS ih24a05.y1 Human insulinoma Homo sapiens cDNA 5' similar to  
DEFINITION TR:Q9ULK6 Q9ULK6 KIAA1214 PROTEIN ; mRNA sequence.  
BM507037  
ACCESSION BM507037.1 GI:18678180  
VERSION EST.  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 557)  
REFERENCE 1  
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
Lemishka, T., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blais, A.,  
Schmitt, A., Theisling, B., Bitter, E., Ronko, L., Bennett, J., Cardenas,  
M., Gibbons, M., McCann, P., Cole, P., Tsagarishvili, P., Williams, T.,  
Jackson, J. and Bowers, Y.  
Endocrine Pancreas Consortium  
Other ESTs: ih24a05.x1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: [dmelton@bioh.harvard.edu](mailto:dmelton@bioh.harvard.edu)  
Library was constructed by Dr. J. Ferrer In vivo mass-excised to  
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington  
University Genome Sequencing Center For information on obtaining a

1358 TAAGTATAGGGAAAGATGAATGGCTCTGGAGGACACGTGCACTCAACAAAT 1412

FINITION Homo sapiens, Similar to hypothetical protein FLJ23516

1357 ATATCTTAATAGTGGCTCTCCCATGAAGAGGATATGCGCAGGACCGCATCATCTGGA 300  
1298 ATATCTTAATAGTGGCTCTCCCATGAAGAGGATATGCGCAGGACCGCATCATCTGGA 300  
241 ATATCTTAATAGTGGCTCTCCCATGAAGAGGATATGCGCAGGACCGCATCATCTGGA 300  
1368 TATGCTTTCATAGAGGGAATGATGAATGGCGCTGTGAGAGAAACGCTGCAGTCAACAAAT 1417







[illegible]

CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: MGC Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCMI354 row: b column: 08  
High quality sequence stop: 655.  
Location/Qualifiers

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source
1. .774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4609831"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B_T1 phage-resistant"

```

SfiI (ggcgctcgcc); Site 2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC library."

268 a 130 c 140 g 236 t

Query Match 21.9%; Score 388; DB 12; Length 774;  
Best Local Similarity 99.8%; Pred. No. 1.4e-207;  
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1256 GAAGATGGATCAGTGTCTTTACAAGTCCCTGTATCCATGAANAATCTCTAATAGTGCCTCC 1315  
|||||  
Db 1 GAAGATGGATCAGTGTCTTTACAAGTCCCTGTATCCATGAANAATCTCTAATAGTGCCTCC 60  
|||||  
QY 1316 TCCCATGAAGAGGATAATCGCAGCGAGCGGATCATCTGGATATGCTTCAGTACAGGGA 1375  
|||||  
Db 61 TCCCATGAAGAGGATAATCGCAGCGAGCGGATCATCTGGATATGCTTCAGTACAGGGA 120  
|||||  
QY 1376 ACAGATGAACGGCCTCTGGAGGAAACACGTGCAGTCAACAAATGAAAGTCTACAGCTGGTA 1435  
|||||  
Db 121 ACAGATGAACGGCCTCTGGAGGAAACACGTGCAGTCAACAAATGAAAGTCTACAGCTGGTA 1480





normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 153 a 244 c 264 g 150 t  
ORIGIN

Query Match 21.2%; Score 376; DB 13; Length 811.  
Best Local Similarity 99.6%; Pred. No. 8.7e-201;  
Matches 476; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 199 GGTCTGCGCAAGCGGTAGCAGGCGCGCTGCCAGGCGGCTAGCAACTGCGGAGCGCGCG 458  
Db 146 GTCTCTGCCAAGCGGTAGCAGGCGCGCTGCCAGGCGGCTAGCAACTGCGGAGCGCGCG 205  
QY 259 CGCATGGGCGCGCGCGCTGGGCGGCGGTCTCTCTGCGCGGCTGCTGCGGCTTTTCCAG 318  
Db 206 CGCATGGGCGCGCGCGCTGGGCGGCGGTCTCTCTGCGCGGCTGCTGCGGCTTTTCCAG 265  
QY 319 ATTGCTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 378  
Db 266 ATTGCTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325  
QY 379 TGAAGCAGTGTGAGCGCGCTACTCAAGTGTGCTGCGGCTTCCGACAGCGAGTGAA 438  
Db 326 TGAAGCAGTGTGAGCGCGCTACTCAAGTGTGCTGCGGCTTCCGACAGCGAGTGAA 385  
QY 439 CCGTACGGTGTGGAGCTGAGCGAGGCGGCTGTACGGGCTAGCACTGCGGCTTGGAGCG 498  
Db 386 CCGTACGGTGTGGAGCTGAGCGAGGCGGCTGTACGGGCTAGCACTGCGGCTTGGAGCG 445  
QY 499 TGTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 558  
Db 446 TGTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505  
QY 559 CAGCAATTTACGGTGGCCACCGTTTGGGAGGACCGTGCAGTCTCTGCTGCTGCTGCTG 618  
Db 506 CAGCAATTTACGGTGGCCACCGTTTGGGAGGACCGTGCAGTCTCTGCTGCTGCTGCTG 565  
QY 619 CATCCAAACCGCGGCGGCTGCGACCTTCGCGAGCAAGATCCATCTGCTTATGAGAGA 676  
Db 566 CATCCAAACCGCGGCGGCTGCGACCTTCGCGAGCAAGATCCATCTGCTTATGAGAGA 623

RESULT 13  
BE958087  
LOCUS 601644929F1 NIH\_MGC\_56 856 bp mRNA linear EST 04-OCT-2000  
DEFINITION mRNA sequence.

ACCESSION BE958087  
VERSION BE958087.1 GI:10568792  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mhc.nci.nih.gov/>.  
National Institutes of Health, Ph.D.

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov

Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.

NIH-MGC Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>  
Plate: LLCM763 row: j column: 07

High quality sequence stop: 635.  
Location/Qualifiers

# FEATURES

## source

1. .856  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3929958"  
/clone\_lib="NIH\_MGC\_56"  
/tissue\_type="primitive neuroectoderm"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ. brain; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggcgctcgcc); Site\_2: SfiI (ggcgctcgcc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCGGCGCGGCGGAGTGT(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 305 a 135 c 173 g 243 t  
ORIGIN

Query Match 21.1%; Score 374; DB 12; Length 856;  
Best Local Similarity 99.8%; Pred. No. 1.2e-199;  
Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1270 GTCTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTCCCTCCCATGAAGAGGA 1329  
Db 44 GTCTTTACAGTCCCTGTATCCAAATGAAATATCTAATAGTCCCTCCCATGAAGAGGA 103

QY 1330 TAATCGCAGGAGACCGCATCATCTGGATATGCTTCACTACAGGAGACAGATGAACGCC 1389  
Db 104 TAATCGCAGGAGACCGCATCATCTGGATATGCTTCACTACAGGAGACAGATGAACGCC 163

QY 1390 TCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTCAGCTGGTGAACCATGAAGCAAA 1449  
Db 164 TCTGGAGGAACACGTCGAGTCAACAAATGAAAGTCTCAGCTGGTGAACCATGAAGCAAA 223

QY 1450 TTCTGTGCGAGTGTATTTATTCCTGATGACACCAACCTTTGAAGAGCAAGAAC 1509  
Db 224 TTCTGTGCGAGTGTATTTATTCCTGATGACACCAACCTTTGAAGAGCAAGAAC 283

QY 1510 TCCTAATCAAGACACTGTGTGCGAGAAATTAATCTTAAATCTGTGTAATAGAAAC 1569  
Db 284 TCCTAATCAAGACACTGTGTGCGAGAAATTAATCTTAAATCTGTGTAATAGAAAC 343

QY 1570 TTGAACCATTAATAACAGAACTGCCAATCAGGGCTAGTTTCTATTATAAATTGGA 1629  
Db 344 TTGAACCATTAATAACAGAACTGCCAATCAGGGCTAGTTTCTATTATAAATTGGA 403

QY 1630 TAAATTTAATAAATAAGTGTAGTACTGAAAGTCTCAGATGACTATATATGCTATAG 1689  
Db 404 TAAATTTAATAAATAAGTGTAGTACTGAAAGTCTCAGATGACTATATATGCTATAG 463

QY 1690 TTAAG 1694  
Db 464 TTAAG 468

RESULT 14  
BE9542034

LOCUS 602060189F1 NIH\_MGC\_58 884 bp mRNA linear EST 11-DEC-2000

DEFINITION mRNA sequence.

ACCESSION BE9542034  
VERSION BE9542034.1 GI:11629415  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mhc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)

REFERENCE 1 (bases 1 to 884)  
AUTHORS NIH-MGC  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I M A G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MQC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCmg88 row: a column: 24  
High quality sequence stop: 536

FEATURES  
SOUND

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1. .884
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:406799"
/clone_lib="NIH_MGC_58"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNP-LIB (Clontech); Site:1:
Sff1 (ggccgcctggccgc); Site_2: Sff1 (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCTCGAGCTCGTCAGATG-df(30)BN-3'
(where B = A, C, G, and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
252 a 179 c 230 g 223 t

```

RESULT 15  
BF66897  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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2	...	...	...	...
3	...	...	...	...
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9	...	...	...	...
10	...	...	...	...
11	...	...	...	...
12	...	...	...	...
13	...	...	...	...
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65	...	...	...	...
66	...	...	...	...
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94	...	...	...	...
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98	...	...	...	...
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100	...	...	...	...

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini, Hominoidea; Homo.  
1 (bases 1 to 879)  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA library preparation: CLONETECH Laboratories, Inc.  
cDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

BASE COUNT  
ORIGIN

```

Query Match      19.7%   Score 349:   DB 12:   Length 879:
Rest local similarity 99.6%:   Pred No. 1.7e-185,
Matches 449:   Conservative 0:   Mismatches 2:   Indels 0:   Gaps 0:

Qy  1244  GAGGTGGATGTTGAAGATGGATCAGTGTCTTTACAAGTCCTCTATCCAATGAAATATCT 1303
Db      1  GAGGTGGATGTTGAAGATGGATCAGTGTCTTTACAAGTCCTCTATCCAATGAAATATCT 60

Qy  1304  AATAGTGGCTTCTTCTTCTATGAAGAGATAATGCGACGAGACCGCATCATCTCGATATGCT 1363
Db      61  AATAGTGGCTTCTTCTTCTTCTATGAAGAGATAATGCGACGAGACCGCATCATCTCGATATGCT 120

Qy  1364  TCAGTACAGGGAAACAGATGAAACCGCTCTCGAGAGAAACCGTGCAGTCAACAATGAAAGT 1423
Db      121  TCAGTACAGGGAAACAGATGAAACCGCTCTCGAGAGAAACCGTGCAGTCAACAATGAAAGT 180

Qy  1424  CTACAGCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCTCATGTGAC 1483
Db      181  CTACAGCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCTCGTGTGAC 240

Qy  1484  AACCCCAACCTTTTGAAGAAGACGAACTCCTAATCAAGAGACTGCTGTTTCGAGAAATTTAA 1543
Db      241  AACCCCAACCTTTTGAAGAAGACGAACTCCTAATCAAGAGACTGCTGTTTCGAGAAATTTAA 300

Qy  1544  TCTTAAATCTGTGTAATAGAAACACTGAACCATTAGTAATACAGAACTGCCAATCAG 1603
Db      301  TCTTAAATCTGTGTAATAGAAACACTGAACCATTAGTAATACAGAACTGCCAATCAG 360

Qy  1604  GGCTTAGTCTTCTATTAAATAAATTTGGATAAATTTAATAAAATAGAGTGCATCTGAAAGTG 1663
Db      361  GGCTTAGTCTTCTATTAAATAAATTTGGATAAATTTAATAAAATAGAGTGCATCTGAAAGTG 420

Qy  1664  CTCAGATGACTAATATTATGCTATAGTTAAA 1694
Db      421  CTCAGATGACTAATATTATGCTATAGTTAAA 480

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/clone="IMAGE:4050022"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCTGAGCGGCGGACAG-3' (30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 145 a 92 c +06 g 123 t
ORIGIN

```

```

Query Match 16.6%; Score 295; DB 12; Length 466;
Best Local Similarity 99.5%; Pred. No. 5.9e-155;
Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1083 GAGATAGTGTGCTGTGATGATGATTAACCAAAATGATTTGGTACGATCTTAA 1142
DB 1 GAGATAGTGTGCTGTGATGATGATTAACCAAAATGATTTGGTACGATCTTAA 60

QY 1143 CGTCACACCATATTTCCATAGACATGCTTACGATGCTGCTTTAAACACAACTT 1202
DB 1 CGTCACACCATATTTCCATAGACATGCTTACGATGCTGCTTTAAACACAACTT 120

QY 1203 GCGCATGTGCAATGTGACATATCTAAAGCTTTTGGGAATTAATGTTGGAAGATG 1262
DB 12 GCGCATGTGCAATGTGACATATCTAAAGCTTTTGGGAATTAATGTTGGAAGATG 180

QY 1263 GATCAGTGTCTTTACAGTGCCTGTATCCAAATGAATATCTATAGTGCCTGCTCCATG 1322
DB 181 GATCAGTGTCTTTACAGTGCCTGTATCCAAATGAATATCTATAGTGCCTGCTCCATG 240

QY 1323 AAGAGGATAATCGCAGGAGACCGCATCTCTGATATGTTTACGACAGGGAACAGATG 1382
DB 241 AAGAGGATAATCGCAGGAGACCGCATCTCTGATATGTTTACGACAGGGAACAGATG 300

QY 1383 AACGCGCTCTGAGACACAGTCGACGTCACAAATGAAAGTCTACAGCTGGTAAACCATG 1442
DB 301 AACGCGCTCTGAGACACAGTCGACGTCACAAATGAAAGTCTACAGCTGGTAAACCATG 360

QY 1443 AAGCAAAATCTGCGAGTGGATGTTTATCTCTCATGT 1479
DB 361 AAGCAAAATCTGCGAGTGGATGTTTATCTCTCATGT 397

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RESULT 24
LOCUS BG400279 759 bp mRNA linear EST 12-MAR-2001
DEFINITION 6024647291 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592897 5'
mRNA sequence.
ACCESSION BG400279
VERSION BG400279.1 GI:13293727
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 759)
AUTHORS NIH-MGC http://imgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1331 row: p column: 18
High quality sequence stop: 736.
FEATURES
source
1..759
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4592897"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCTGAGCGGCGGACAG-3' (30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 250 a 141 c 141 g 227 t
ORIGIN

```

```

Query Match 16.6%; Score 294; DB 12; Length 759;
Best Local Similarity 99.7%; Pred. No. 2.3e-154.
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1224 TACTCAAGCTTTGGGAATGAGTGGATGATTTCAAGATGATGATGCTTTTACAGTCC 1283
DB 1 TACTCAAGCTTTGGGAATGAGTGGATGATTTCAAGATGATGATGCTTTTACAGTCC 60

QY 1284 CTGTATCCAAATGAATATTAATAGTGGCTCCCATGATGAGGAGATATATCCAGCGAGA 1343
DB 61 CTGTATCCAAATGAATATTAATAGTGGCTCCCATGATGAGGAGATATATCCAGCGAGA 120

QY 1344 CCGCATCATCTGATATGCTTCAGTACAGGAGACACATCAACCGCTCTGGAGGAACAG 1403
DB 121 CCGCATCATCTGATATGCTTCAGTACAGGAGACACATCAACCGCTCTGGAGGAACAG 180

QY 1404 TGCAGTCAACAAATGAAGTCTACAGCTGGTAAACCATGATGATGCTGGCAGTGG 1463
DB 181 TGCAGTCAACAAATGAAGTCTACAGCTGGTAAACCATGATGATGCTGGCAGTGG 240

QY 1464 ATGTTATTCCTCATGTCAGCAACCCAACTTTGAAGAACACGAACTCTTAATCAAGAGA 1523
DB 241 ATGTTATTCCTCATGTCAGCAACCCAACTTTGAAGAACACGAACTCTTAATCAAGAGA 300

QY 1524 CTGCTGTTTCGAGAAATTAATCTTAAATCTGTGTAATAGAGAA 1568
DB 301 CTGCTGTTTCGAGAAATTAATCTTAAATCTGTGTAATAGAGAA 345

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```

RESULT 25
LOCUS BI715115 482 bp mRNA linear EST 19-SEP-2001
DEFINITION ic29b03.y1 HR85 islet Homo sapiens cDNA 5' mRNA sequence.
ACCESSION BI715115
VERSION BI715115.1 GI:15690810
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 482)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
TITLE

```





Db	438	GTTCAGATGACTAATTAATGCTATAGTAA	469
RESULT 27			
H48650		458 bp	mRNA
LOCUS			linear
DEFINITION			EST 15-SEP-1995
			Yr33b01.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone
			IMAGE:207044 5' similar to SP-30-11-UG-OME 20500; GOLIATH PROTEIN ;
			mRNA sequence.
ACCESSION			H48650
VERSION			H48650
KEYWORDS			EST.
SOURCE			H48650.1 GI:988490
ORGANISM			human.
			Homo sapiens
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE			1 (bases 1 to 458)
AUTHORS			Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
			M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, T.
			Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
			R., Williamson, A., Wohldmann, P. and Wilson, R.
TITLE			The Washu-Merck EST Project
JOURNAL			Unpublished (1995)
COMMENT			Contact: Wilson RK
			Washington University School of Medicine
			4444 Forest Park Parkway, Box 8501, St Louis, MO 63108
			Tel: 314 286 1800
			Fax: 314 286 1810
			Email: est@watson.wustl.edu
			Insert Size: 1435
			High quality sequence stops: 300
			Source: IMAGE Consortium, LNL
			This clone is available royalty-free through LNL; contact the
			IMAGE Consortium (info@image.llnl.gov) for further information.
			Insert Length: 1435 Std Error: 0.00
			Seq Primer: M13RP1
			High quality sequence stop: 300.
FEATURES			source
			Location/Qualifiers
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			/db_xref="taxon:9606"
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			/sex="male"
			/dev_stage="20 week-post conception fetus"
			/lab_host="DH10B (ampicillin resistant)"
			/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
			with a modified polylinker; Site_1: Pac 1; Site_2: Eco RI;
			1st strand cDNA was primed with a Pac 1 - oligo(dT) primer
			[5' AACGAGCAATTAATAAGACATTTTTTTTTTTTTTTT 3'].
			Double-stranded cDNA was ligated to Eco RI adaptors
			(Pharmacia), digested with Pac 1 and cloned into the Pac 1
			and Eco RI sites of the modified pT7T3 vector. Library
			went through one round of normalization. Library
			constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT			133 a 92 c 105 g 123 t 5 others
ORIGIN			
Query Match			14.4%; Score 256; DB 14; Length 458;
Best Local Similarity			99.4%; Pred. No. 6.9e-133;
Matches			356; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1080	ATGGAGATAGTGTGCTGTGCTATTAATGCTATTAACCAAAATGATTTGGTACGATCT	1139
Db	1	ATGGAGATAGTGTGCTGTGCTATTAATGCTATTAACCAAAATGATTTGGTACGATCT	60
QY	1140	TAACTGCAACCATATTTTCCATTAAGACATGTGTGTGACCATGCTGCTTAAACACACAGA	1199
Db	61	TAACTGCAACCATATTTTCCATTAAGACATGTGTGTGACCATGCTGCTTAAACACACAGA	120
QY	1200	CTTGCCCATGTGCAATGTGCATATCTCAAAGCTTTTGGAAATTTGAGTGGATTTGAAG	1259
Db	1	CTTGCCCATGTGCAATGTGCATATCTCAAAGCTTTTGGAAATTTGAGTGGATTTGAAG	1018



QY 1339 CGAGACCGCATATCTGGATATGCTTCAGTACAGGGAACAGATGAACCCCTCTGGAGGA 1398  
 Db 61 CGAGACCGCATATCTGGATATGCTTCAGTACAGGGAACAGATGAACCCCTCTGGAGGA 120  
 QY 1399 ACAGCTGCTACACAAATGAAGTCTACAGCTGGTAAACCATGAGCAAAATCTCTGCGC 1458  
 Db 121 ACAGCTGCTACACAAATGAAGTCTACAGCTGGTAAACCATGAGCAAAATCTCTGCGC 180  
 QY 1459 AGTGGATTTATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1517  
 Db 181 AGTGGATTTATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
 QY 1518 AAGAGCTGCTGTGTCAGAAATTAATCTTAAATCTGTGTAATAGAAACTTGAACCA 1577  
 Db 241 AAGAGCTGCTGTGTCAGAAATTAATCTTAAATCTGTGTAATAGAAACTTGAACCA 200  
 QY 1578 TTACTATAACAGAGTGGTCAAGGCTAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1637  
 Db 301 TTACTATAACAGAGTGGTCAAGGCTAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360  
 QY 1638 ATAAATAGAGAGTATGATCAAGAGTGTCTCAGATGACTAAT 1677  
 Db 361 ATAAATAGAGAGTATGATCAAGAGTGTCTCAGATGACTAAT 400  
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 LOCUS le65f05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
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 ACCESSION BI964160  
 VERSION BI964160.1 GI:16338565  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 545)  
 REFERENCE  
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ponko,I., Bennett,J., Cardenas  
 M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,P., Williams,T.,  
 Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Published (2000)  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Juliana Brown  
 (brownjefas.harvard.edu) This sequence now available from the IMAGE  
 consortium, for clone orders contact: info@image.llnl.gov  
 High quality sequence stop: 437.  
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 /tissue\_type="Islets of Langerhans"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B"  
 /note="Organ: Pancreas; Vector: pSPORT1; Site:1; Not 1;  
 Site\_2: Sal 1; Starting library constructed using

Superscript Plasmid Library kit (Life Technologies). cDNA  
 made by oligo-dr priming. Size-selected by column  
 fractionation: average insert size 1.08 kb. Library was  
 amplified once on solid support and plasmid DNA from  
 library was prepared. The library DNA was normalized by  
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
 Research 6:791-806; 0.5 microgram single-stranded library  
 plasmid DNA was mixed with 5 micrograms PCR product  
 representing library inserts and hybridized to an EcoT of  
 20. Single-stranded (unhybridized) plasmids were isolated  
 by hydroxyapatite chromatography and used to make this  
 library.

BASE COUNT 189 a 85 c 83 g 188 t  
 ORIGIN  
 Query Match 12.8% Score 2271 DB 13 Length 545.  
 Best Local Similarity 99.6% Pred. No. 1.8e-116;  
 Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1417 TGAAGCTTACAGCTGGTAAACCATGAGCAAAATCTGTGGCAGTGGATGTTATTCCTCA 1476  
 Db 1 TGAAGCTTACAGCTGGTAAACCATGAGCAAAATCTGTGGCAGTGGATGTTATTCCTCA 60  
 QY 1477 TGTGACACACCCACCTTTGAAGACAGACAACTCTTAATCAAGAGACTGCTGTTCGAGA 1536  
 Db 61 TGTGACACACCCACCTTTGAAGACAGACAACTCTTAATCAAGAGACTGCTGTTCGAGA 120  
 QY 1537 AATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATTTAGTAATAACAGAACTGC 1596  
 Db 121 AATTAATCTTAAATCTGTGTAATAGAAAACCTTGAACCATTTAGTAATAACAGAACTGC 180  
 QY 1597 CAATCAGGCGCTAGTTTCTTATTAATAAATTTGATGATAATTAATAAATTAAGAGTGATCT 1656  
 Db 181 CAATCAGGCGCTAGTTTCTTATTAATAAATTTGATGATAATTAATAAATTAAGAGTGATCT 240  
 QY 1657 GAAAGTCTCAGACTGACTAATATATGCTATAGTTAAA 1694  
 Db 241 GAAAGTCTCAGACTGACTAATATATGCTATAGTTAAA 278  
 T50929 358 bp mRNA linear EST 06-FEB-1995  
 YB8E02.rl Stratagene liver (#937224) Homo sapiens cDNA clone  
 IMAGE:78266 5', mRNA sequence.  
 T50929 31:652789  
 VERSION T50929.1  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 358)  
 REFERENCE  
 AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins  
 M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,F., Moore  
 B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,  
 Schellenberg,K., Soares,M.R., Tan,F., Thierry-Mieg,J., Trevaskis,E.,  
 Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)  
 9704478  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 260  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: M13RP1



JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM927 row: i column: 19  
High quality sequence stop: 602.  
Location/Qualifiers  
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/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: Brain; Vector: pDRP-LIR (Clontech); Site\_1: SfiI (ggcgctcgcc); Site\_2: SfiI (ggcattatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGGCGGAGCGGCGGACATG-dl(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."  
BASE COUNT 249 a 120 c 139 g 224 t

FEATURES  
source

Query Match 12.5% Score 221; DB 12; Length 732.  
Best Local Similarity 100.0%; Pred. No. 4.7e-113;  
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1255 TGAAGATGGATCAGTCTTTTACAGTCCCTGATCCCAATGAATATTTATATGTCCTC 1314  
Db 11 TGAAGATGGATCAGTCTTTTACAGTCCCTGATCCCAATGAATATTTATATGTCCTC 70  
QY 1315 CTCCCATGAAGAGATATCGGAGGAGACCCGATCATCTGGATATGCTTCAGTACAGGG 1374  
Db 71 CTCCCATGAAGAGATATCGGAGGAGACCCGATCATCTGGATATGCTTCAGTACAGGG 130  
QY 1375 AACATGATGAACGCTCTCGAGAGAACACCTGTCAGTCAACAATGAAATGATATGCT 1474  
Db 131 AACATGATGAACGCTCTCGAGAGAACACCTGTCAGTCAACAATGAAATGATATGCT 190  
QY 1435 AAACCATGAAGCAAAATTCGTGGCAGTGGATGTTATTCCTC 1475  
Db 191 AAACCATGAAGCAAAATTCGTGGCAGTGGATGTTATTCCTC 231

RESULT 35  
D60241  
LOCUS

DEFINITION 400 bp mRNA linear EST 28-AUG-1995  
HUM093005B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-094605 5', mRNA sequence.  
ACCESSION D60241  
VERSION D60241.1 GI:961880  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 400)  
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S., and Nakamura, Y.  
TITLE Fujiwara et al. (1995)

## TITLE

Fujiwara et al. (1995)

JOURNAL  
COMMENT

Unpublished (1995)  
Contact: Tsutomu Fujiwara  
Otsuka GEN Research Institute  
Otsuka Pharmaceutical Co., Ltd  
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan  
Tel: 0886-65-2888  
Fax: 0886-37-1035.  
Location/Qualifiers  
1. 400  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GEN-093G05"  
/clone\_lib="Clontech human fetal brain polyA+ mRNA (#6535)"  
/note="Male adult, hematopoietic tissue, stem cell"  
BASE COUNT 146 a 70 c 61 g 123 t

FEATURES  
source

Query Match 12.4% Score 220; DB 14; Length 400;  
Best Local Similarity 99.6%; Pred. No. 1.6e-112;  
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1424 CTACAGCTGTAACCATCAACCAATTCCTGCGAGTGGATGTTATTCCTCATGTGAC 1483  
Db 8 CTACAGCTGTAACCATCAACCAATTCCTGCGAGTGGATGTTATTCCTCATGTGAC 67  
QY 1484 AACCCCAACCTTGAAGAACACCACTCTAATCAAGAGACTGCTGTCGAGAAATATAA 1543  
Db 68 AACCCCAACCTTGAAGAACACCACTCTAATCAAGAGACTGCTGTCGAGAAATATAA 127  
QY 1544 TCTTAAATCTGTGTAATAGAAACCTTGACCATTAAGACAGACTGCCAATCAG 1603  
Db 128 TCTTAAATCTGTGTAATAGAAACCTTGACCATTAAGACAGACTGCCAATCAG 187  
QY 1604 GGCTAGTCTTCTATTAAATAATGGATAATTTAATAAATGAAGTGTACTGAAAGTG 1663  
Db 188 GGCTAGTCTTCTATTAAATAATGGATAATTTAATAAATGAAGTGTACTGAAAGTG 247  
QY 1664 CTCAGATGACTAATATTATGCTATAGTTAAA 1694  
Db 248 CTCAGATGACTAATATTATGCTATAGTTAAA 278

RESULT 36  
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LOCUS

DEFINITION 876 bp mRNA linear EST 21-DEC-2000  
H2124238F1 NIH\_MGC\_56 Homo sapiens cDNA clone IMAGE:4381345 5', mRNA sequence.  
ACCESSION BF665797  
VERSION BF665797.1 GI:11939692  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgc.ncbi.nlm.nih.gov/  
1 (bases 1 to 876)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM1109 row: k column: 10  
High quality sequence stop: 605.  
Location/Qualifiers  
1. .876  
/organism="Homo sapiens"

FEATURES  
source

Query Match 12.4% Score 220; DB 14; Length 400;  
Best Local Similarity 99.6%; Pred. No. 1.6e-112;  
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1424 CTACAGCTGTAACCATCAACCAATTCCTGCGAGTGGATGTTATTCCTCATGTGAC 1483  
Db 8 CTACAGCTGTAACCATCAACCAATTCCTGCGAGTGGATGTTATTCCTCATGTGAC 67  
QY 1484 AACCCCAACCTTGAAGAACACCACTCTAATCAAGAGACTGCTGTCGAGAAATATAA 1543  
Db 68 AACCCCAACCTTGAAGAACACCACTCTAATCAAGAGACTGCTGTCGAGAAATATAA 127  
QY 1544 TCTTAAATCTGTGTAATAGAAACCTTGACCATTAAGACAGACTGCCAATCAG 1603  
Db 128 TCTTAAATCTGTGTAATAGAAACCTTGACCATTAAGACAGACTGCCAATCAG 187  
QY 1604 GGCTAGTCTTCTATTAAATAATGGATAATTTAATAAATGAAGTGTACTGAAAGTG 1663  
Db 188 GGCTAGTCTTCTATTAAATAATGGATAATTTAATAAATGAAGTGTACTGAAAGTG 247  
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source

1. .807  
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/issue\_type="primitive neuroectoderm"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site: 1:  
SfiI (ggcccctggccc); Site 2: SfiI (ggccattatggccc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCCGACATG-dT(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 271 a 152 c 127 g 256 t 1 others  
ORIGIN

Query Match 12.1% Score 214; DB 12; Length 807;  
Best Local Similarity 100.0%; Pred. No. 4.3e-109;  
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 GATACATCAAGTCTTGAAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTCGAGCAATT 1540  
DB 47 GATACATCAAGTCTTGAAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTCGAGCAATT 106  
QY 1541 AATCTTAAATCTGTGTAATAGAAACCTTGAACCATTTAGTAATAAAGAACTGCTCAAT 1600  
DB 107 AATCTTAAATCTGTGTAATAGAAACCTTGAACCATTTAGTAATAAAGAACTGCTCAAT 166  
QY 1601 CAGGCGCTACTTCTTATTAATTAATGCAATAAATTAATAAATAGAGTACTGTAAT 1660  
DB 167 CAGGCGCTACTTCTTATTAATTAATGCAATAAATTAATAAATAGAGTACTGTAAT 226  
QY 1661 GTCTCAGATGATTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1694  
DB 227 GTCTCAGATGATTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 260

RESULT 38  
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LOCUS 602125574F1 NIH\_MGC\_56 Homo sapiens cDNA clone IMAGE:4282339 5',  
DEFINITION mRNA sequence.  
ACCESSION BF698234  
VERSION BF698234.1 GI:11983642  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 938)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL112 row 3 column 29  
High quality sequence stop: 604.  
Location/Qualifiers  
1. .938  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

FEATURES  
source

BASE COUNT 288 a 140 c 187 g 261 t

ORIGIN

Query Match 12.4% Score 220; DB 12; Length 876;  
Best Local Similarity 99.6%; Pred. No. 1.8e-112;  
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1389 CTCTGAGAGAACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1448  
DB 89 CTCTGAGAGAACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 148  
QY 1449 ATTCTGTGAGTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1508  
DB 149 ATTCTGTGAGTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 208  
QY 1509 CTCTTAATCAAGATCTGTTTGAAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTCGAGCAATT 1568  
DB 209 CTCTTAATCAAGATCTGTTTGAAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTCGAGCAATT 258  
QY 1569 CTCTTAATCAAGATCTGTTTGAAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTCGAGCAATT 1628  
DB 269 CTCTTAATCAAGATCTGTTTGAAGAGAGAGAACTCTTAATCAAGAGACTGCTGTTCGAGCAATT 328  
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DB 329 ATAAATTTAAATAAAGAGTACTGTAAT 359

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DEFINITION mRNA sequence.  
ACCESSION BF701837  
VERSION BF701837.1 GI:11987245  
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 807)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL120 row 5 column 16  
High quality sequence start: 21  
High quality sequence stop: 615.  
Location/Qualifiers

FEATURES







```

source 1. .462
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5637219"
/clone_lib="Human Pancreatic Islets"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/notes="Organ: Pancreas; Vector: pSPORT1; Site: 1; Not 1; Site: 2; Sal 1; Library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size selected by column fractionation, average insert size 1.08 kb. Primary library, unamplified."

BASE COUNT 139 a 84 c 107 g 130 t 2 others
ORIGIN
Query Match 10 1%; Score 179; DB 10; Length 462;
Best Local Similarity 99.1%; Pred. No. 2.7e-89;
Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 852 AAAACATGCGCTTGGGTGAATATATTAATTTTTCCTTCTGCTTTTAA 911
|||||
Db 69 AAAACATGCGCTTGGGTGAATATATTAATTTTTCCTTCTGCTTTTAA 128
|||||

QY 912 TTATACGGCGCAACTGGGCTATTTATCTTTTATCTGCTGAAGGCTACGAATG 971
|||||
Db 129 TTATACGGCGCAACTGGGCTATTTATCTTTTATCTGCTGAAGGCTACGAATG 188
|||||

QY 972 CAAGAGCTTAAGCAGGAGGAGCAATTAAGGCGAGATCTAAAGAACTATTGGA 1031
|||||
Db 189 CAGAGCTCAAGCAGGAGGAGCAATTAAGGCGAGATCTAAAGAACTATTGGA 248
|||||

QY 1032 GGCTTCACTACGACACTGAACAGGAGAGCAAGAAATGGCCCTGATGGAGATGTT 1091
|||||
Db 249 GGCTTCACTACGACACTGAACAGGAGAGCAAGAAATGGCCCTGATGGAGATGTT 308
|||||

QY 1092 GTGCTGTGCTCAATGATTAACCAAAATGATTTGTCAGGCGATCTTAAGTGCAC 1151
|||||
Db 309 GTGCTGTGCTCAATGATTAACCAAAATGATTTGTCAGGCGATCTTAAGTGCAC 368
|||||

QY 1152 ATATTTCCATAAGACATGTGTGACCCCATGG 1183
|||||
Db 369 ATATTTCCATAAGACATGTGTGACCCCATGG 400
|||||

RESULT 43
R24902
LOCUS yh38d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
DEFINITION IMAGE:132015 5', mRNA sequence.
ACCESSION R24902
VERSION R24902 1 GI:779790
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 368)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maizumi, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1362
High quality sequence stops: 190

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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1362 Std Error: 0.00
Seq primer: M13Rpl
High quality sequence stop: 190.
Location/Qualifiers
1. .368
/organism="Homo sapiens"
/db_xref="GDB:537571"
/db_xref="taxon:9606"
/clone="IMAGE:132015"
/clone_lib="Soares placenta Nb2HP"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker, Site 1, Not 1, Site 2, Eco RI, 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AACTGGAAGAATCCGCGCCGAGGAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 107 a 77 c 89 g 95 t
ORIGIN
Query Match 9.9%; Score 176; DB 14; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.3e-87;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1253 GTTGAAGATGGATCAGTGTCTTTTACAAGTCCCTGTATCCAATGAATATCTAATAGTCC 1312
|||||
Db 1 GTTGAAGATGGATCAGTGTCTTTTACAAGTCCCTGTATCCAATGAATATCTAATAGTCC 60
|||||

QY 1313 TCTCTCCATGAGAGGATTAATCGCAGCGAGCCGATCATCTGGATGCTTCAGTACAG 1372
|||||
Db 61 TCTCTCCATGAGAGGATTAATCGCAGCGAGCCGATCATCTGGATGCTTCAGTACAG 120
|||||

QY 1373 GGAACAGATGAACCGCTCTGGAGGAGAACGTCGAGTCAACAAATGAAGTCTACA 1428
|||||
Db 121 GGAACAGATGAACCGCTCTGGAGGAGAACGTCGAGTCAACAAATGAAGTCTACA 176
|||||

RESULT 44
BE958612
LOCUS 601645258P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930207 5',
DEFINITION mRNA sequence.
ACCESSION BE958612
VERSION BE958612.1 GI:10569317
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM764 row: d column: 16
High quality sequence stop: 560.
Location/Qualifiers

```

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source
1. .561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3930207"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="PH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pNMR-LIB (Clontech); Site_1: SfiI (ggccattatgcc); Site_2: SfiI (ggccattatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 197 a 84 c 86 g 194 t
ORIGIN

Query Match 9.2%; Score 163; DB 12; Length 561;
Best Local Similarity 99.5%; Pred. No. 3.1e-80;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 GACACCCACACCTTTGAAGAGACGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 1540
Db 6 GACACCCACACCTTTGAAGAGACGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 65

Qy 1541 AAATCTTTAAATCTGTATAATAGAAAACCTTGAACCAATTAGTAATCAAGAACTGCCAAT 1600
Db 66 AAATCTTTAAATCTGTATAATAGAAAACCTTGAACCAATTAGTAATCAAGAACTGCCAAT 125

Qy 1601 CAGGCGCTAGTTCTATTATAATAGTAATAGTAATTTAATAAATAGAGTACTGATACTGAAA 1660
Db 126 CAGGCGCTAGTTCTATTATAATAGTAATAGTAATTTAATAAATAGAGTACTGATACTGAAA 185

Qy 1661 GTGCTCAGTACTAATATTATGCTATAGTTAAA 1694
Db 186 GTGCTCAGTACTAATATTATGCTATAGTTAAA 219

RESULT 45
BF666952
LOCUS BF666952 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930207, 855 bp mRNA linear EST 21-DEC-2000
DEFINITION BF666952.1 GI:11940847
ACCESSION BF666952
VERSION BF666952.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 855)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph D.
Email: rgs@biml.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium/LLNL at: http://image.llnl.gov
Plate: L1CM1102 row: n column: 24
High quality sequence stop: 603.
Location/Qualifiers
1. .855
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone_lib="IMAGE:4278743"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="PH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pNMR-LIB (Clontech); Site_1: SfiI (ggccattatgcc); Site_2: SfiI (ggccattatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 232 a 171 c 168 g 284 t
ORIGIN

Query Match 9.2%; Score 163; DB 12; Length 855;
Best Local Similarity 99.5%; Pred. No. 3.2e-80;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 GACACCCACACCTTTGAAGAGACGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 1540
Db 43 GACACCCACACCTTTGAAGAGACGAACTCTTAATCAAGAGACTGCTGTTGAGAAAT 102

Qy 1541 AAATCTTTAAATCTGTATAATAGAAAACCTTGAACCAATTAGTAATCAAGAACTGCCAAT 1600
Db 103 AAATCTTTAAATCTGTATAATAGAAAACCTTGAACCAATTAGTAATCAAGAACTGCCAAT 162

Qy 1601 CAGGCGCTAGTTCTATTATAATAGTAATAGTAATTTAATAAATAGAGTACTGATACTGAAA 1660
Db 163 CAGGCGCTAGTTCTATTATAATAGTAATAGTAATTTAATAAATAGAGTACTGATACTGAAA 222

Qy 1661 GTGCTCAGTACTAATATTATGCTATAGTTAAA 1694
Db 223 GTGCTCAGTACTAATATTATGCTATAGTTAAA 256

RESULT 46
BF666952
LOCUS BF666952 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278743, 855 bp mRNA linear EST 30-SEP-1996
DEFINITION BF666952.1 GI:11940847
ACCESSION BF666952
VERSION BF666952.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 224)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1995)
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawachi-cho, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
Location/Qualifiers
1. .224
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4278743"
/clone_lib="NIH_MGC_56"
/notes="Male adult, hematopoietic tissue, stem cell"
BASE COUNT 83 a 38 c 37 g 63 t
ORIGIN

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Query Match      9.1%; Score 161; DB 14; Length 224;
Best Local Similarity 100.0%; Pred. No. 3 9e-79;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 GACAAACCAACCTTGAAGAGAGAGAACTCCCTAAATCAAGAGACTCTGTGTGAGAAATT 1540
|||||
DB 64 GACAAATCAAGCTTTTGAAGAGAGAGAACTCCCTAAATCAAGAGACTCTGTGTGAGAAATT 123
|||||

QY 1541 AAATCTTAAATCTGTGTAATATAAATAAATCTGAACCATTAATTAACAGAACTGCAAT 1600
|||||
DB 124 AAATCTTAAATCTGTGTAATATAAATAAATCTGAACCATTAATTAACAGAACTGCAAT 183
|||||

QY 1601 CAGGCGCTAGTTCTTATTAATAATTAATGGATAAATTTAATAA 1641
|||||
DB 184 CAGGCGCTAGTTCTTATTAATAAATTAATGGATAAATTTAATAA 224
|||||

RESULT 47
LOCUS BF664617 904 bp mRNA linear EST 21-DEC-2000
DEFINITION 602117401P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4274977 5'.
mRNA sequence.
ACCESSION BF664617
VERSION BF664617.1 GI:11938512
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI093 row: b column: 02
High quality sequence stop: 584.
FEATURES
source
location/Qualifiers
1..904
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/notes="Organ: brain; Vector: PNP-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcgctatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 272 a 190 c 196 g 244 t 2 others
ORIGIN
Query Match      8.9%; Score 158; DB 12; Length 904;
Best Local Similarity 100.0%; Pred. No. 2.2e-77;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1032 GGGTTCAACTACGCACTGAAACAAAGGAGACAAAGAAATGGCCCTGATGAGATAGTT 60
|||||
DB 1092 GTCGTGTGTGTAATGTAATTAATAACCAATGTTGTAGCATCTTTAAAGCTGCAACC 1151
|||||
DB 61 GTCGTGTGTGTAATGTAATTAATAACCAATGTTGTAGCATCTTTAAAGCTGCAACC 120
|||||
QY 1152 ATATTTTCCATAGATATGATGTTGATGATGATGATGATGATGATGATGATGATGAT 1189
|||||
DB 121 ATATTTTCCATAGATATGATGTTGATGATGATGATGATGATGATGATGATGATGAT 158
|||||

RESULT 48
LOCUS BE536963 445 bp mRNA linear EST 09-AUG-2000
DEFINITION 601064790F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450983 5'.
mRNA sequence.
ACCESSION BE536963
VERSION BE536963.1 GI:9765608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8430 row: d column: 24
High quality sequence stop: 445.
FEATURES
source
location/Qualifiers
1..445
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT 152 a 63 c 64 g 166 t
ORIGIN
Query Match      8.5%; Score 150; DB 10; Length 445;
Best Local Similarity 100.0%; Pred. No. 6.9e-73;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1545 CTTAAATCTGTGTAATGAAACCTTGAAACCATTAAGTAATACAGAACTGCCAATCAGG 1604
|||||
DB 1 CTTAAATCTGTGTAATGAAACCTTGAAACCATTAAGTAATACAGAACTGCCAATCAGG 60
|||||
QY 1605 GCCTAGTCTTCTATTATAAATTTGGATAAATTTAATAAATAAGAGTGATGATGAAAGTGC 1664
|||||
DB 61 GCCTAGTCTTCTATTATAAATTTGGATAAATTTAATAAATAAGAGTGATGATGAAAGTGC 120
|||||
QY 1665 TCAGATGACTAATATTATGCTATAGTTAAA 1694
|||||
DB 121 TCAGATGACTAATATTATGCTATAGTTAAA 150
|||||

RESULT 49
LOCUS BF032034 769 bp mRNA linear EST 10-OCT-2000

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DEFINITION 601559604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:382297 5',
            mRNA sequence.
ACCESSION  BF032034
VERSION    BF032034.1 GI:10739746
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 769)
AUTHORS   NIH-MGC http://mgc.nhl.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L10CM501 row: h column: 62
            High quality sequence stop: 523.
FEATURES   source
            Location/Qualifiers
                1..769
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:382297"
                /clone_11b="NIH_MGC_58"
                /tissue_type="hypertrophoma"
                /lab_host="DH10B (TI phage-resistant)"
                /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggc);
                Double-stranded cDNA was prepared from cell line RNA. 5'
                and 3' adaptors were used in cloning as follows: 5'
                adaptor sequence: 5'-CAAGGCGATTATGCCC-3' and 3' adaptor
                sequence: 5'-ATTCTAGAGCGGCGGCGGCGCATG-dr(30)BN-3'
                (where B = A, C, G, or T). Average
                insert size 1.35 kb (range 0.9-4.0 kb). 15/35 colonies
                contained inserts by PCR. This library was enriched for
                full-length clones and was constructed by Clontech
                Laboratories (Palo Alto, CA)."
BASE COUNT  236 a 164 c 127 g 242 t
ORIGIN
Query Match      8.2%; Score 145; DB 12; Length 769;
Best Local Similarity 100.0%; Pred. No. 4.9e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 GACACCCCAACCTTTGAAGAGAGCAAACTCTAATCAAGAGACTGCTGTTCGAGAAAT 1540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 55 GACAACTCAATCTTTGAAGAGAGCAAACTCTAATCAAGAGACTGCTGTTCGAGAAAT 114

QY 1541 AAATCTTAAATCTGTGTAATAGAAAACCTGAACTTATTATTAATAGAACTTGTCAAT 1600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 115 AAATCTTAAATCTGTGTAATAGAAAACCTTGAACCAATTAGTAATACAGAACTGCAAT 174

QY 1601 CAGGCGCTAGTCTTCTATTAATAAAT 1625
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 175 CAGGCGCTAGTCTTCTATTAATAAAT 199

RESULT 50
BG960989/c
LOCUS      BG960989
DEFINITION PM2-CT0265-170401-014-d05 CT0265 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG960989
VERSION    BG960989.1 GI:14374160
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE  1 (bases 1 to 304)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,P.R., Peis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc Natl Acad Sci U S A 97 (7), 4491-4496 (2000)
MEDLINE    20202653
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2at2-PM2-CT0265-
            170401-014-d05&t3=2001-04-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 15
            High quality sequence stop: 286.
FEATURES   source
            Location/Qualifiers
                1..304
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_11b="CT0265"
                /dev_stage="Adult"
                /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                SmaI; A mini-library was made by cloning products derived
                from ORESTES PCR (U.S. Letters Patent application No. 196
                ,716 - Ludwig Institute for Cancer Research) profiles
                into the puc 18 vector. Reverse transcription of tissue
                mRNA and cDNA amplification were performed under low
                stringency conditions."
BASE COUNT  88 a 69 c 55 g 92 t
ORIGIN
Query Match      7.6%; Score 135; DB 13; Length 304;
Best Local Similarity 99.5%; Pred. No. 2.1e-64;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 TGTGGCTATTTTATCTTTTATCTGCTCGAAGGCTACGGAATGCAAGAGCTCAAGACAG 987
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 245 TGTGGCTATTTTATCTTTTATCTGCTCGAAGGCTACGGAATGCAAGAGCTCAAGACAG 186

QY 988 GAAGCAGAGGCAATTAAGGCAGATGCTAAAAAGCTTATGGAAGCTTCAACTAGGCAC 1047
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 195 GAAGCAGAGGCAATTAAGGCAGATGCTAAAAAGCTTATGGAAGCTTCAACTAGGCAC 126

QY 1048 ACTGAACACAGGACAGCAAGAAATTCGCCCTGATGAGATAGTTGTCTGTGCAATCA 1107
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 125 ACTGATACAGGAGACAGCAAGAAATTCGCCCTGATGAGATAGTTGTCTGTGCAATCA 66

QY 1108 ATTGTA 1113
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Db 65 ATTGTA 60

Search completed: October 31, 2002, 11:44:19
Job time : 2040 secs

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GenCore version 5.1.1  
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OM nucleic - nucleic search, using sw model

Run on: October 31 2002 08:56:14 : Search time 270 Seconds  
(without alignments)  
14796.463 Million cell updates/sec

Title: US-09-854-100-7

Perfect score: 1774  
Sequence: 1 agctgagctacacgggt.....ataggaaagttctctctctg tttg

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database: N\_Geneseq\_101002.\*  
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Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1774	100.0	1774	24	AAI72095 Human GRAIL cDNA
2	1417	79.9	2773	21	AAAI5995 Human protein clem
3	1417	79.9	2796	24	AAI72321 ISIGP 4 cDNA, Hom
4	1080	60.9	1284	21	AAAI5985 Human protein clem
5	824	46.4	2306	22	AAS25884 Human cDNA encoding
6	790	44.5	1135	22	AAI59292 Human polynucleoti
7	722	40.7	1249	24	ABL90796 Human polynucleoti
8	704	39.7	1250	22	ABL26340 Human cDNA encoding
9	497	29.0	2476	22	AAS45511 Human cDNA encoding

#### ALIGNMENTS

RESULT: 1  
AAI72095

10	360	20.3	737	22	AAI61078 Human polynucleoti
11	354	20.0	502	24	ABN19991 Human ORFX polynuc
12	292	16.5	404	22	AAF66696 Novel human polynu
13	275	15.5	646	24	ABL38246 Human colon tumour
14	167	9.4	435	24	ABK45625 cDNA encoding colo
15	80	4.5	922	22	AAF78996 Human secreted pro
16	78	4.4	810	21	AAC59154 Human secreted pro
17	78	4.4	1055	24	ABQ54249 Human ovarian anti
18	77	4.3	912	21	AA232934 Human acrosomal sp
19	77	4.3	1568	23	ABK43706 DNA encoding novel
20	76	4.3	387	22	AAH35391 Human colon cancer
21	76	4.3	613	22	AAH33228 Human colon cancer
22	76	4.3	940	22	ABA77069 Proliferative glom
23	76	4.3	1247	22	AAH35001 Human colon cancer
24	76	4.3	1772	22	ABA06482 Human cDNA SEQ ID
25	76	4.3	2776	24	ABL52661 cDNA encoding nove
26	76	4.3	3789	22	AAS26981 Human immune/haema
27	75	4.2	373	22	AAK59576 Human immune/haema
28	75	4.2	411	22	AAK60386 Human secreted pro
29	75	4.2	558	21	AAC80580 Human secreted pro
30	75	4.2	745	21	AAA87692 Human nervous syst
31	75	4.2	829	23	ABAI12886 Human polynucleoti
32	75	4.2	846	24	ABL90566 Proliferative glom
33	75	4.2	864	22	ABA77055 Human secreted pro
34	75	4.2	882	21	AAC63454 Human cDNA encoding
35	75	4.2	1243	22	AAS33285 Human cDNA SEQ ID
36	75	4.2	1355	22	ABA06738 Human polynucleoti
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38	75	4.2	1355	22	AAI63957 Human polynucleoti
39	75	4.2	1355	22	AAS31368 Human cDNA encoding
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41	75	4.2	1355	24	ABQ66692 Human polynucleoti
42	75	4.2	1591	22	AAS12087 Human tumour necro
43	75	4.2	1605	21	AAA71141 Human Adipose Spec
44	75	4.2	1744	22	AAS7734 cDNA encoding nove
45	75	4.2	1802	21	AA248809 Soybean inositol 1
46	75	4.2	2005	24	ABL23256 Human secreted pro
47	75	4.2	2099	22	AAAL2681 Human reproductive
48	75	4.2	2099	23	ABL97322 Human testicular a
49	75	4.2	200	22	AAH35162 Human colon cancer
50	74	4.2	247	22	AAH35170 Human colon cancer
51	74	4.2	258	22	AAH67823 Peppermint plant o
52	74	4.2	433	22	AAH35061 Human colon cancer
53	74	4.2	463	22	ABAI1343 Human nervous syst
54	74	4.2	485	22	ABA07627 Human ovarian and
55	74	4.2	485	22	AAO2322 Human reproductive
56	74	4.2	492	21	AAO78292 Human cancer assoc
57	74	4.2	524	20	AAH30385 DNA encoding a hum
58	74	4.2	552	24	ABQ54502 Human ovarian anti
59	74	4.2	559	22	AAH34635 Human colon cancer
60	74	4.2	560	24	ABL32390 Human secreted pro
61	74	4.2	572	22	AAK59622 Human immune/haema
62	74	4.2	604	22	AAAL3358 Human secreted pro
63	74	4.2	608	21	AAAB1134 Human secreted pro
64	74	4.2	612	24	ABQ54522 Human ovarian anti
65	74	4.2	640	22	ABAO7535 Human ovarian and
66	74	4.2	640	22	AAAL00464 Human reproductive
67	74	4.2	640	23	ABK72059 Human cDNA encoding
68	74	4.2	660	24	ABK91651 cDNA encoding nove
69	74	4.2	663	22	AAK60757 Human immune/haema
70	74	4.2	687	20	AAH30321 DNA encoding a hum
71	74	4.2	707	22	AAI98650 Human excretory re
72	74	4.2	707	22	AAI63046 Human kidney relat
73	74	4.2	736	24	ABL90752 Human polynucleoti
74	74	4.2	737	22	ABL99590 Human expressed po
75	74	4.2	737	22	ABA06066 Human cDNA SEQ ID

ID AA172095 standard; cDNA: 1774 BP.  
 AC AA172095;  
 DT 25-MAR-2002 (first entry)  
 DE Human GRAIL cDNA.  
 KW Murine; human; GRAIL; anergy; attenuation; tyrosine phosphorylation;  
 KW antigenic stimulation; interleukin-2; gene therapy; polymorphism; IL-2;  
 KW autoimmune disease; tumour cells; cancer; transplant rejection; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 263..1547  
 FT /\*tag= a  
 FT /product= "GRAIL"  
 PH WC200195243.A1  
 XX 15-NOV-2001  
 XX 11-MAY-2001: 2601W-H-15385  
 XX 11-MAY-2000: 2000US-203513P.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR  
 PI Ford GS, Bloom D, Fathman GS;  
 DR WPI: 2002-055597/07  
 DR P-PSDR: AAR47800.  
 XX Novel nucleic acid sequences of anergy associated genes, including  
 PT GRAIL gene useful in the evaluation of pathophysiology of immunotherapy  
 PT of cancer, autoimmune disease and transplant rejection -  
 PS Claim 2: Page 45-47: 50pp: English.  
 CC This sequence encodes human GRAIL protein. The GRAIL gene is an  
 CC anergy associated gene which is upregulated during the early stages of  
 CC induction of anergy. GRAIL has been shown to attenuate IL-2  
 CC transcription in T-cells during response to antigenic stimulation.  
 CC GRAIL DNA is useful for decreasing the responsiveness of a T cell  
 CC population, especially synthesis of interleukin-2 (IL-2) in response to  
 CC antigenic stimulation, by up-regulating GRAIL activity in the T cell  
 CC population. GRAIL DNA is useful in producing compositions that modulate  
 CC induction or maintenance of anergy, for gene therapy, mapping  
 CC functional regions of the encoded protein, to analyse a patient sample  
 CC for the presence of polymorphisms or alterations in expression of  
 CC sequences associated with T cell anergy, disease states, genetic  
 CC predisposition to a disease state, and in studying associated  
 CC physiological pathways. Modulation of the gene activity in vivo is  
 CC useful for prophylactic and therapeutic purposes, such as treating  
 CC autoimmune disease and to enhance immune response to tumour cells, and  
 CC identification of anergic T cells. GRAIL DNA is useful in the  
 CC evaluation of the pathophysiology or immunotherapy of cancer,  
 CC autoimmune disease, and transplant rejection. Genetic sequences  
 CC involved in anergy induction are useful as markers in the evaluation of  
 CC specific immunotherapies. Functional characterization of genes involved  
 CC in anergy induction allows the elucidation of the mechanisms of T cell  
 CC anergy, including the transcriptional blockade of IL-2, which may be  
 CC manipulated to regulate T cell responses in human disease. Modulation  
 CC of expression of GRAIL gene is useful in manipulating the anergic  
 CC state. The genetic sequences find use alone or in combinations in  
 CC determining the expression profile of cells relating to anergy, for  
 CC example in screening of candidate biologically active compounds for  
 CC modulation of T cell anergy. Expression of GRAIL has been found to  
 CC block tyrosine phosphorylation of a protein present in T cells during  
 CC activation.  
 XX Sequence 1774 BP: 454 A: 432 C: 464 G: 423 T: 1 other:

Query Match	100.0%	Score 1774:	DB 24:	Length 1774:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches 1774:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY	1	AGCTGGAGTCCACACGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGCGCGAGG	60	
DB	1	AGCTGGAGTCCACACGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGCGAGG	60	
QY	61	AATTCGGCAAGACGCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGCGAGG	120	
DB	61	AATTCGGCAAGACGCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGCGAGG	120	
QY	121	CCTGGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGAGG	180	
DB	121	CCTGGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGAGG	180	
QY	181	GGCACTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGAGG	240	
DB	181	GGCACTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGAGG	240	
QY	241	GGCACTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGAGG	300	
DB	241	GGCACTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGCGAGG	300	
QY	361	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	360	
DB	361	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	360	
QY	361	ACCGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	420	
DB	361	ACCGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	420	
QY	421	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	480	
DB	421	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	480	
QY	481	GGCACTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	540	
DB	481	GGCACTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	540	
QY	541	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	600	
DB	541	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	600	
QY	601	AGTTCCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	660	
DB	601	AGTTCCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	660	
QY	661	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	720	
DB	661	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	720	
QY	721	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	780	
DB	721	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	780	
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DB	781	TGGCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	840	
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DB	841	AGTTCCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	900	
QY	901	AGTTCCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	960	
DB	901	AGTTCCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	960	
QY	961	AGTTCCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	1020	
DB	961	AGTTCCTGGCGCGCTGGCACTAGTGCATCCCGCGCGTGGCGCGCTAGAACTAGTGCATCCCGCGCGAGG	1020	

QY	1021	AGCTATTGGAAAGGTTCAACTACAGCAATATGAACAAGAGAGAACAGAAGTAATTCAGGCTGA	1090
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DB	1021	AGCTATTGGAAAGGTTCAACTACAGCAATATGAACAAGAGAGAACAGAAGTAATTCAGGCTGA	1089
QY	1081	TGGAGATAGTGTGTCGTGTGTTGATTAATATGATAAACCAGATGATTTGCCTATCGCATCTT	1140
DB			
DB	1081	TGGAGATAGTGTGTCGTGTGTTGATTAATATGATAAACCAGATGATTTGCCTATCGCATCTT	1140
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DB			
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QY	1201	TTGCCCCATGTGCCAAATGTGACATATCTCAACACITTTGSCAATTTGAGTGTGSAATGTAACA	1260
DB			
DB	1201	TTGCCCCATGTGCCAAATGTGACATATCTCAACACITTTGSGAATTTGAGTGTGSAATGTAACA	1260
QY	1261	TGSATCAGTGTCTTTACAAAGTGCCCTGATGCCAATGAAATATCTAATAGTCCCTCTCCCA	1320
DB			
DB	1261	TGSATCAGTGTCTTTACAAAGTGCCCTGATGCCAATGAAATATCTAATAGTCCCTCTCCCA	1320
QY	1321	TGAAGAGGATATGCTATGCAAGATGCGATCATTTGATATATCTTTCAGATACAGGCAACACA	1380
DB			
DB	1321	TGAAGAGGATATGCTATGCAAGATGCGATCATTTGATATATCTTTCAGATACAGGCAACACA	1380
QY	1381	TGAACCGCTCTTGAGGAACACGTGTGASTTAACTAATGSAAGTCTACAGCTGGSTAAACCA	1440
DB			
DB	1381	TGAACCGCTCTTGAGGAACACGTGTGASTTAACTAATGSAAGTCTACAGCTGGSTAAACCA	1440
QY	1441	TGAAGCAAAATCTGTGCGAGTGTGATGTTATTTCTTATPNTGACAGCAACAGCCTTTGAGA	1500
DB			
DB	1441	TGAAGCAAAATCTGTGCGAGTGTGATGTTATTTCTTATPNTGACAGCAACAGCCTTTGAGA	1500
QY	1501	AGACGAAAACCTCCTAATCAAGAGAGCTGCTGTCGAGAAATTAATCTTAAATCTGTGTAA	1560
DB			
DB	1501	AGACGAAAACCTCCTAATCAAGAGAGCTGCTGTCGAGAAATTAATCTTAAATCTGTGTAA	1560
QY	1561	ATAGAAAACTTTGACACCATTAGTAAATACACAAATTTGACACAGCGCTTATGTTTCTTAA	1620
DB			
DB	1561	ATAGAAAACTTTGACACCATTAGTAAATACACAAATTTGACACAGCGCTTATGTTTCTTAA	1620
QY	1621	TAAATTCGATATAATTTAATAAATAAGATGTATATGAAAGTGGTCCAGATGATTAATATT	1680
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QY	1681	ATGCTATAGTTAAATGGCTTAAAAATATTTAACCTGTAACTTTTTCCACCAAACTCA	1740
DB			
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QY	1741	TTATATAATTTTTCATAGCAAGTTTCCTCTCAG	1774
DB			
DB	1741	TTATATAATTTTTCATAGCAAGTTTCCTCTCAG	1774
RESULT 2			
ID	AAAL15995		
XX	AAAL15995 standard; cDNA; 2773 BP.		
AC	AAAL15995;		
XX			
DT	(first entry)		
XX	Human protein clone HP10574 full length coding sequence.		
DE			
XX			
KW	Human protein; hydrophobic domain; nutritional source; haematopoiesis;		
KW	cytokine production; cell proliferation; cell differentiation;		
KW	immune deficiency; infectious disease; autoimmune disorder; asthma;		
KW	multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;		
KW	allergic reaction; osteoporosis; osteoarthritis; periodontal disease;		
KW	nervous system disorder; Alzheimer's disease; Parkinson's disease;		
KW	Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;		
KW	systemic cytokine damage; tissue differentiation; contraceptive; stroke;		
KW	regulation disorder; myocardial infarction; inflammatory condition;		
KW	septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;		

KW	nephritis; therapy; ss.
XX	
QS	Homo sapiens.
PN	W52000005367.A2.
XX	
PD	03-FEB-2000.
XX	
FF	22-JUL-1999; 99WO-JR08
XX	
XX	27-AUG-1998; 98JP-0202
FF	04-JUL-1998; 98JP-0202
PR	25-AUG-1998; 98JP-0202
FF	09-SEP-1998; 98JP-0259
PR	29-SEP-1998; 98JP-0270
XX	
PA	(SAGA) SAGAMI CHEM RES
PA	(PROT-) PROTEGENE INC.
XX	
PI	Kato S, Kimura T;
DR	WPI: 2000-182694/16.
NP	P-FSDB: AAY4897.
XX	
PT	Novel human proteins hav
PT	osteoporosis, Alzheimers
PT	multiple sclerosis, rheu
XX	
PS	Claim 4; Page 348-351;
XX	
CC	This sequence encodes a
CC	hydrophobic domains. The
CC	genetic marker. The pro
CC	potential genetic disor
CC	nutritional sources or
CC	proliferation, cell diffe
CC	other cytokines in cert
CC	immune stimulating or i
CC	treatment of various im
CC	infectious diseases cau
CC	infections. The protein
CC	such as multiple sclero
CC	arthritis. It is also u
CC	conditions such as asth
CC	transplantation. The pr
CC	and consequently in the
CC	deficiencies. It is als
CC	tissues, and conditions
CC	also used for promoting
CC	activities and as a fert
CC	treating various coagula
CC	conditions resulting fr
CC	infarction or stroke. T
CC	inhibitors or agonists
CC	treat inflammatory cond
CC	reperfusion injury, art
CC	prevent tumours.
XX	
SU	Sequence 2773 BP; 803 A
	Query Match 79%
	Best Local Similarity 99%
	Matches 161; Conservative
CV	74 CGAGGAGGTCATCTCTCT

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Query Match          79.9%  Score 1417,  DB 21,  Length 2773;
Best Local Similarity 99.8%  Pred. No. 0;
Matches 117;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;
CY  74  CCAGAGAGCTGCATCTGAGTAACTCTGTGTCTGACGTAAGTCTGCTGCTGCTGACG 133

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PR 08-NOV-2000; 2000US-0246524.  
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 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246529.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246560.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246615.  
 PR 17-NOV-2000; 2000US-0246267.  
 PR 17-NOV-2000; 2000US-0246208.  
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 PR 17-NOV-2000; 2000US-0249211.  
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 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249400.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250161.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251044.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 05-DEC-2000; 2000US-0251474.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251860.  
 PR 08-DEC-2000; 2000US-0251864.  
 PR 08-DEC-2000; 2000US-0251900.  
 PR 11-DEC-2000; 2000US-0254197.  
 PR 05-JAN-2001; 2001US-0254078.  
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-488783/53.

XX F-PSUB; AAU15897.

PT New nucleic acid molecules encoding 461 human secreted proteins for  
 PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives.

PS Claim 1: SEQ ID NO 63; 48899; English.

XX The invention relates to isolated nucleic acid molecules and their  
 CC encoded secreted proteins. The nucleic acids and proteins are used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
 CC are also used in diagnosing a pathological condition or susceptibility  
 CC to a pathological condition. Antibodies to the proteins can also  
 CC be used in alleviating symptoms associated with the disorders and in  
 CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
 CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated  
 CC include autoimmune diseases e.g. rheumatoid arthritis,  
 CC hyperlipidemia, disorders e.g. nephrosis of the kidney, liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
 CC and ocular disorders e.g. corneal infection, and many other  
 CC disorders listed in the specification. The polypeptides can also  
 CC be used to aid wound healing and epithelial cell proliferation, to

CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence encodes a novel secreted protein of the invention.

Query Match 45.4%; Score 824; DB 22; Length 2306;  
 Best Local Similarity 99.8%; Pred NO. 0;  
 Matches 1144; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 547 CTGTAAACCCGACACGAAATTCACGGTGGCCAGAGTTTGGAGAGCAATGTAAGTCTTC 606  
 DB 12 CTGTAAACCCGACACGAAATTCACGGTGGCCAGAGTTTGGAGAGCAATGTAAGTCTTC 71  
 QY 507 TTGGTTGGGCTTCATCCACGCGGAGGAGGAGTTCACACCTTGGCAGAGCAATGTCGC 666  
 DB 72 TTGGTTGGGCTTCATCCACGCGGAGGAGGAGTTCACACCTTGGCAGAGCAATGTCGC 131  
 QY 567 TTATGAGAGATGGGGGCTCTGGAGGAGGAGTTCATTTAACTTGGGAGAGGAGTCTTC 726  
 DB 132 TTATGAGAGATGGGGGCTCTGGAGGAGGAGTTCATTTAACTTGGGAGAGGAGTCTTC 191  
 QY 727 CATCCCATATCTCTACCCCGGGTGGCAATATGTTGTAATCATCATGATGGGCAATCTGAA 786  
 DB 192 CATCCCATATCTCTACCCCGGGTGGCAATATGTTGTAATCATCATGATGGGCAATCTGAA 251  
 QY 787 AGGCACAAAATCTGTAATCTATTCAAAACAGGATATAAAGTCACAAATGGTATATAAGCT 846  
 DB 352 AGGCACAAAATCTGTAATCTATTCAAAACAGGATATAAAGTCACAAATGGTATATAAGCT 311  
 QY 847 AGGCACAAAATCTGTAATCTATTCAAAACAGGATATAAAGTCACAAATGGTATATAAGCT 905  
 DB 312 AGGCACAAAATCTGTAATCTATTCAAAACAGGATATAAAGTCACAAATGGTATATAAGCT 371  
 QY 905 TTCTTATATATACGGGCGCAATCTGGGCTATTTATCTTTATCTTCTGTAAGGCTAT 965  
 DB 372 TTCTTATATATACGGGCGCAATCTGGGCTATTTATCTTTATCTTCTGTAAGGCTAT 431  
 QY 965 GSAATGTAAGAGTCAAGAGCAGGAGCAGGCAATTAAGAGCAGGAGTCTTAAGAGCTA 1025  
 DB 432 GSAATGTAAGAGTCAAGAGCAGGAGCAGGCAATTAAGAGCAGGAGTCTTAAGAGCTA 491  
 QY 1026 TTGAGAGGCTTCAACTACGCACACTGAAACAGAGGAGCAAGAAATGGCCCTGATGGAG 1085  
 DB 492 TTGAGAGGCTTCAACTACGCACACTGAAACAGAGGAGCAAGAAATGGCCCTGATGGAG 551  
 QY 1086 ATAGTTGCTGCTGTGCTATGCAATGTTATATAACCAATATATGTTACGCACTTAAAGCT 1145  
 DB 552 ATAGTTGCTGCTGTGCTATGCAATGTTATATAACCAATATATGTTACGCACTTAAAGCT 611  
 QY 1146 GCAACCATATTTCCCATAGACATGTTGTGACCCATGGGCTGTTTAAACACAGAGCTTGC 1205  
 DB 612 GCAACCATATTTCCCATAGACATGTTGTGACCCATGGGCTGTTTAAACACAGAGCTTGC 671  
 QY 1206 GATATGTAATGAGTATATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 1265  
 DB 672 GATATGTAATGAGTATATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 731  
 QY 1265 GATATGTAATGAGTATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 1325  
 DB 732 GATATGTAATGAGTATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 791  
 QY 1325 GATATGTAATGAGTATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 1385  
 DB 792 GATATGTAATGAGTATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 851  
 QY 1385 GATATGTAATGAGTATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 1445  
 DB 852 GATATGTAATGAGTATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 911  
 QY 1445 GATATGTAATGAGTATATCAATCAAGGTTTGGGAATTTAGSTGATGTTGAGCTGAT 1505



QY 1592 ACTGCCAATCAGGCGCTAGTCTTCTATTATAAATTGATATAATTTTAAATAAAGCTG 1651  
 Db 911 ACTGCCAATCAGGCGCTAGTCTTCTATTATAAATTGATATAATTTTAAATAAAGCTG 970  
 QY 1652 ATACTGAATGCTCAGATGACTAATATTATGCTATAGTTAA 1694  
 Db 971 ATACTGAATGCTCAGATGACTAATATTATGCTATAGTTAA 1013

RESULT 7  
 ABL90796  
 ID ABL90796 standard; cDNA; 1249 bp.  
 XX  
 AC ABL90796;  
 XX  
 DT 24-MAY-2002 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 1358.  
 XX  
 FW cytostatic; immunosuppressive; antitumor; neuroprotective; antiviral;  
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein; gene; ss  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200190304-A2.  
 XX  
 FD 29-NOV-2001.  
 XX  
 PF 18-MAY-2001; 2001WO-US16450  
 XX  
 PR 19-MAY-2000; 2000US-205515P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI IN  
 XX  
 PI Birse CE, Rosen CA;  
 DR WPI: 2002-1225-A,16.  
 DR P-PSDB: ABB90387.  
 XX  
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
 PT prevention of neural, immune system, muscular, reproductive,  
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
 PT disorders.  
 XX  
 PS Claim 4; SEQ ID NO 1358. 2001pp - Sequence listing: English.  
 XX  
 CC The invention relates to novel genes (AB90449-AB90453) and proteins  
 CC (AB90440-AB90444) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral ataxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 CC Note. The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.  
 XX  
 SQ Sequence 1249 bp; 379 A; 258 C; 273 G; 335 T; 4 other;  
 Query Match 40.7%; Score 722; DB 24; Length 1249;  
 Best Local Similarity 99.4%; Pred No H.

	Matches 1142;	Conservative	0;	Mismatches	6;	Indels	1;	Gaps	1;
QY	547	CTGTACCCGACACAGAAATTTTACGGTGCCTCCAGCGTTTGGGGAACACCGTGCAGATCTC	606						
Db	18	CTGTAAACCCGACACAGAAATTTTACGGTGCCTCCAGCGTTTGGGGAACACCGTGCAGATCTC	77						
QY	607	TTGGTTGGGCTTTTATCAACATGGGCGGCGGCTGACCTTTCAGACACAGATTCATCTGGG	666						
Db	78	TTGGTTGGGCTTTTATCAACATGGGCGGCGGCTGACCTTTCAGACACAGATTCATCTGGG	137						
QY	667	TTATGAGAGATGGGCGGCTTGGAGCGGCTTAACTTTCCCGGACCGCCGCAATGAGGT	726						
Db	138	TTATGAGAGATGGGCGGCTTGGAGCGGCTTAACTTTCCCGGACCGCCGCAATGAGGT	197						
QY	727	CATCCCGCATGTCTCACCCGGGTGCAGTACACATTTGTTGCAATCATGATCGGCAATCTGAA	786						
Db	198	CATCCCGCATGTCTCACCCGGGTGCAGTACACATTTGTTGCAATCATGATCGGCAATCTGAA	257						
QY	787	AGGCACAAAAATTTCTGCAATCTATTCAAGAGGCATACAAAGTGACAATGGTGCATAGAAGT	846						
Db	258	AGGCACAAAAATTTCTGCAATCTATTCAAGAGGCATACAAAGTGACAATGGTGCATAGAAGT	317						
QY	847	AGGGAACAAACATGGCGGCTTGGGTGAATCACTATTCAATTTTTTTCGTTTCTGTCTCCT	906						
Db	318	AGGGAACAAACATGGCGGCTTGGGTGAATCACTATTCAATTTTTTTCGTTTCTGTCTCCT	377						
QY	907	TTTTTATTATACGGCGGCACTGTGGGCTATTTTATCTTTTATCTGCTCGAAGGCTAGG	966						
Db	378	TTTTTATTATACGGCGGCACTGTGGGCTATTTTATCTTTTATCTGCTCGAAGGCTAGG	437						
QY	967	GAATGCAAGAGCTCAAAAGCAGGAGCAGCAATTAAGAGGAGATGCTAAAAAGCTAT	1026						
Db	438	GAATGCAAGAGCTCAAAAGCAGGAGCAGCAATTAAGAGGAGATGCTAAAAAGCTAT	497						
QY	1027	TGGAGAGCTTCACTAGGCACACTGAAACAGAGAGCAGG-AAATTGGCCCTGATGAG	1085						
Db	498	TGGAGAGCTTCACTAGGCACACTGAAACAGAGAGCAGG-AAATTGGCCCTGATGAG	557						
QY	1086	ATAGTTGTGCTGTGCTGATTTGAATTTATATAAATCAATTTGATGCTGATGATGAG	1145						
Db	558	ATAGTTGTGCTGTGCTGATTTGAATTTATATAAATCAATTTGATGCTGATGATGAG	617						
QY	1146	GCACCATATTTTCCATATAGACATGTGTTGACCCATGCTGTTAAACACACAGACTTCC	1205						
Db	618	GCACCATATTTTCCATATAGACATGTGTTGACCCATGCTGTTAAACACACAGACTTCC	677						
QY	1206	CCATGTGCAAAATGTGACATACCTCAAAAGCTTTGGGAATTCAGGTGATGTTGAAGATG	1265						
Db	678	CCATGTGCAAAATGTGACATACCTCAAAAGCTTTGGGAATTCAGGTGATGTTGAAGATG	737						
QY	1266	CAGTGTCTTTTACAGCTGCTTCTATCAATCAATCAATCAATCAATCAATCAATCAAT	1325						
Db	738	CAGTGTCTTTTACAGCTGCTTCTATCAATCAATCAATCAATCAATCAATCAATCAAT	797						
QY	1326	AGCATATGTCAGGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	1385						
Db	798	AGCATATGTCAGGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	857						
QY	1386	CCATGTGCAAAATGTGACATACCTCAAAAGCTTTGGGAATTCAGGTGATGTTGAAGATG	1445						
Db	858	CCATGTGCAAAATGTGACATACCTCAAAAGCTTTGGGAATTCAGGTGATGTTGAAGATG	917						
QY	1446	CAATTTCTGTCAGGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	1505						
Db	918	CAATTTCTGTCAGGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	977						
QY	1506	AAATCTCTTAATCAAGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	1565						
Db	978	AAATCTCTTAATCAAGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	1037						
QY	1566	AAATCTCTTAATCAAGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	1625						
Db	1038	AAATCTCTTAATCAAGAGAGCGGATCATCTGGATATGCTTCAGTACAGAGGACAGATGAC	1097						

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OY 1626 TGGATAAATTAATAAATAAGAGTGATCTGAAAGTGTCTGAGATGACTAATATTATGCT 1685
Db 1098 TGGATAAATTAATAAATAAGAGTGATCTGAAAGTGTCTGAGATGACTAATATTATGCT 1157
OY 1686 ATAGTTAAA 1694
Db 1158 ATAGTTAAA 1166

RESULT 8
ID AAS26340
XX AAS26340 standard; cDNA; 1250 bp
AC AAS26340;
XX
DT 07-NOV-2001 (first entry)
DE Human cDNA encoding a novel secreted protein, Seq ID 519.
XX
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW cytotatic; cardiac; vasotropic; cerebroprotective; neotropic;
KW neuroprotective; antibacterial; virucide, fungicide; ophthalmological;
KW vulnary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN W0200155322-A2.
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-0501341.
XX
PR 31-JAN-2000; 2000US-0170065.
PR 04-FEB-2000; 2000US-0180029.
PR 24-FEB-2000; 2000US-0184064.
PR 02-MAR-2000; 2000US-0185050.
PR 16-MAR-2000; 2000US-0189974.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0190123.
PR 19-APR-2000; 2000US-0205515.
PR 02-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214086.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216547.
PR 07-JUL-2000; 2000US-0216580.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218293.
PR 26-JUL-2000; 2000US-0220973.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225277.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 15-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226281.
PR 22-AUG-2000; 2000US-0226869.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227000.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246603.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
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Db 371 TAAATAGAAAACCTGAACCACTAGTAGTAATACAGA 404

RESULT 13  
ABL38226  
ID ABL38226 standard; cDNA: 646 BP.  
XX  
AC ABL38226;  
XX  
DT 08-APR-2002 (first entry)  
XX  
DE Human colon tumour antigen polynucleotide SEQ ID NO:1815.  
XX  
KW Human; colon cancer; colon tumour antigen; cytostatic; vaccine;  
KW colon tumour metastatic antigen; diagnosis; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200196388-A2.  
XX  
PU 20-DEC-2001.  
XX  
XX 08-JUN-2001: 2001WO-US18557  
XX  
PR 09-JUN-2000: 2000US-210899P  
PR 20-FEB-2001: 2001US-270216P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Jiang Y, Harlocker SL, Secrist H;  
XX  
DR WPI: 2002-114514/15.  
XX  
XX Novel isolated colon tumor polynucleotide differentially expressed in  
PT colon tumor or colon metastatic tumor and polypeptides encoded by them,  
PT useful for inhibiting development of cancer in patient.  
XX  
PS Claim 1: SEQ ID 1815: 105pp; English.  
XX  
XX ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)  
CC which were isolated from human colon tumour and colon metastatic tumour  
CC cDNA libraries. (I) have cytostatic activity and can be used in vaccine  
CC production. (I) can be used for stimulating and/or expanding T cells  
CC specific for a tumour protein on contact with the T cells. They are also  
CC useful for inhibiting the development of cancer in a patient. (I) can be  
CC used as probes or primers for nucleic acid hybridisation, for preparing  
CC mutant species primers, or primers for use in genetic constructions. (I)  
CC can be used in the diagnosis of a colon tumour.  
XX  
SQ Sequence 646 BP; 226 A; 103 C; 106 G; 208 T; 3 other;

Query Match 15.5%, Score 275, DB 24, Length 646;  
Best Local Similarity 99.7%; Pred. No. 8.3e 129;  
Matches 325; Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1369 ACAGTGAACATGAATGCTCTGAGGAAATGCTGATTAACAAATGAAAGTCTACA 1428  
Db 1 ACAGGAGACATATTAAGAGGCTGATGAGGAAACAGCTGACGACAAATGAAAGTCTACA 60  
QY 1429 GCTGTAAACCATGAAGCAAAATCTGCTGGACGTGATGTTATTCCTCATGTGACACAC 1489  
Db 61 GCTGTAAACCATGAAGCAAAATCTGCTGGACGTGATGTTATTCCTCATGTGACACAC 149  
QY 1489 ACCCTTTTAAAGAACGAAACTCTTAATCAAGACACTGCTGTCGAGCAAAATTAATCTTA 1549  
Db 121 ACCCTTTTAAAGAACGAAACTCTTAATCAAGACACTGCTGTCGAGCAAAATTAATCTTA 190  
QY 1549 AAATCTGTGAATAGAAAACCTTGAACCATTAATTAATCAAGAACTGCTGAATCAGGAGCT 1608  
Db 181 AAATCTGTGAATAGAAAACCTTGAACCATTAATTAATCAAGAACTGCTGAATCAGGAGCT 140  
QY 1609 AGTTCTCTATTAAATAAATGGATAAATTTAATAAATAAGAGTGTATGAAAGTGTCTCA 1609

Db 241 AGTTTCTATTAAATAATGGATAAATTTAATAAATAAGAGTGATAGTGAAGTGCTCAG 300

QY 1669 ATGACTAATATTATGCTATAGTTAAA 1694  
|||||  
Db 301 ATGACTAATATTATGCTATAGTTAAA 326  
|||||

RESULT 14  
ABK45625/C  
ID ABK45625 standard; cDNA: 435 BP.  
XX  
AC ABK45625;  
XX  
DT 05-JUN-2002 (first entry)  
XX  
DE cDNA encoding colon tumour protein, SEQ ID NO 1176.  
XX  
KW Human; colon tumour; vaccine; colon cancer; immunogenic;  
KW immunotherapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200212328-A2.  
XX  
FD 14-FEB-2002.  
XX  
PF 31-JUL-2001: 2001WO-US24218.  
XX  
PR 03-AUG-2000: 2000US-223283P.  
PR 28-MAR-2001: 2001US-279763P.  
PR 29-JUN-2001: 2001US-302051P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX King GE, Meagher MJ, Xu J, Secrist H;  
XX  
DR WPI: 2002-241739/29.  
XX  
XX New colon cancer polypeptides and polynucleotides, useful as vaccines,  
PT for diagnosing, preventing, and treating colon cancer, and as markers  
PT for the progression of cancer.  
XX  
PS Claim 1: SEQ ID NO 1176: 147pp; English.  
XX  
XX The invention relates to polynucleotides encoding colon tumour proteins.  
CC The polynucleotides and encoded polypeptides are useful in pharmaceutical  
CC compositions, such as vaccines, for the diagnosis, prevention, and  
CC treatment of colon cancer. Polynucleotide sequences may be used as  
CC hybridisation probes or primers, and in the design and preparation of  
CC ribozyme molecules for inhibiting expression of tumour polypeptides and  
CC proteins in tumour cells. The compositions are useful for stimulating an  
CC immune response against cancer, particularly for the immunotherapy of  
CC colon cancer, and as markers for the progression of cancer.  
CC  
CC ABK4450-ABK4647 represent coding sequences of human colon tumour  
CC proteins of the invention.  
CC Note: With the exception of SEQ ID NO.1 and 2, the sequence data  
CC for this patent did not form part of the printed specification but was  
CC supplied by the European Patent Office.  
XX  
SQ Sequence 435 BP; 147 A; 62 C; 69 G; 157 T; 0 other;

Query Match 9.4%, Score 167, DB 24, Length 435;  
Best Local Similarity 100.0%; Pred. No. 4.6e-74;  
Matches 167; Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1528 TGTTTCGAGAATTAATPCTTAAATCTGTGTAATAAGAAAACCTGAAACCATTAAGTAA 1587  
|||||  
Db 337 TGTTTCGAGAATTAATPCTTAAATCTGTGTAATAAGAAAACCTGAAACCATTAAGTAA 278  
|||||

QY 1588 CAGAACTGCCAAATCAGGGGCTAGTTCTCTATTAATAAATGGATAAATTTAATAAATAAG 1647  
|||||  
Db 277 CAGAACTGCCAAATCAGGGGCTAGTTCTCTATTAATAAATGGATAAATTTAATAAATAAG 218  
|||||

QY 1648 AGTGATCTGAAAGTCTCAGATGACTAATATTATGCTATAGTTAAA 1694  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 217 AGTGATCTGAAAGTCTCAGATGACTAATATTATGCTATAGTTAAA 171

## RESULT 15

AAF97896  
 ID AAF97896 standard; cDNA: 922 BP.

XX AAF97896;  
 XX

DT 01-JUN-2001 (first entry)  
 XX

DE Human secreted protein cDNA, SEQ ID NO: 23.  
 XX

XX Human: secreted protein; immunomodulatory; antisclerotic;  
 KW dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant;  
 KW vascular; anti-angiogenic; ophthalmological; neuroprotectant;  
 KW neurotropic; anticonvulsant; antialzheimers; antiparkinsonian;  
 KW antimicrobial; vulnerary; vaccine; gene therapy; cancer;  
 KW protein coordinate data; infection; ss.  
 XX

OS Homo sapiens.  
 XX

PN WC200121658-A1.  
 XX

PD 29-MAR-2001.  
 XX

PF 22-SEP-2000; 2000WO-US26013.  
 XX

PR 24-SEP-1999; 99US-0155709.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX

PI Ni J, Baker KP, Ririse CE, Ebner P, Fiscella M, Komatsoulis GA;  
 PI Lafleur DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR;  
 PI Young PE, Wei P, Florence KA;  
 XX

DR WPI: 2001-235311/24.  
 XX

PT Nucleic acids encoding 32 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's  
 PT disease and diabetic retinopathy -  
 XX

PS Claim 1: Page 728; 890pp; English.  
 XX

CC The present sequence encodes one of 32 novel human secreted polypeptides.  
 CC The nucleic acid molecules and polypeptides they encode may be used in  
 CC the prevention, diagnosis and treatment of diseases such as  
 CC immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus  
 CC and human immuno-deficiency virus (HIV) infections), hyperproliferative  
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases  
 CC (e.g. Schmitz syndrome, Chaga's cardiomyopathy and coronary  
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft  
 CC neovascularisation and diabetic retinopathy), neurological disorders  
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),  
 CC infectious diseases and/or for promoting wound healing, regeneration  
 CC and/or chemotaxis. The nucleic acid molecules may be used to produce the  
 CC secreted polypeptides. They may also be used as cDNA probes in diagnostic  
 CC assays to detect and quantitate the presence of similar nucleic acid  
 CC sequences in samples. The polypeptides may be used as antigens in the  
 CC production of antibodies and in assays to identify modulators of  
 CC their expression and activity.  
 XX

SQ Sequence 922 BP; 272 A; 198 G; 230 C; 203 T; 4 other;

Query Match 4.5%, Score 80, DR 22, Length 922.  
 Best Local Similarity 100.0%; Pred. No. 5,9e-30;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCATGAGTGGTGGGCGGCTCTAGCAATAGTGGATCCCGGCGCTGACG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 35 AGCTGGAGTTCATGAGTGGTGGGCGGCTCTAGCAATAGTGGATCCCGGCGCTGACG 94

QY 61 AATTGGCAGCAGCGCAGGA 80  
 ||||||||||||||||||||  
 Db 95 AATTGGCAGCAGCGCAGGA 114

## RESULT 16

AAC59154  
 ID AAC59154 standard; cDNA: 810 BP.

XX AAC59154;  
 AC

DT 02-FEB-2001 (first entry)  
 XX

DE Human secreted protein coding sequence, SEQ ID NO: 57.  
 XX

XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;  
 KW antiallergic, hepatotropic, antidiabetic, antiinflammatory, antitumor,  
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein; ss.  
 XX

OS Homo sapiens.  
 XX

PN WC2000055177-A2.  
 XX

PD 21-SEP-2000.  
 XX

PF 09-MAR-2000; 2000WO-US86058.  
 XX

PR 12-MAR-1999; 99US-0124145.  
 XX

PR 03-DEC-1999; 99US-0168634.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX

PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX

DR WPI: 2000-638177/61.  
 XX

DR P-PSDB: AAB28058.  
 XX

PT Novel nucleic acids encoding 49 human secreted proteins useful for  
 PT treating cancers, hyperproliferative disorders, inflammatory disorders,  
 PT neurological disorders and cardiovascular disorders -  
 XX

PS Claim 1: Page 345; 389pp; English.  
 XX

CC The invention relates to the isolation of genes AAS9108-A59156 encoding  
 CC 49 human secreted proteins AAB28012-B28060. The genes can be used to  
 CC generate fusion proteins by linking to the gene for the human  
 CC immunoglobulin G Fc portion (SEQID1) for increasing the stability of  
 CC the fusion protein as compared to the human protein only. The genes and  
 CC proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated  
 CC from a range of human tissues disclosed in the specification. The  
 CC nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)  
 CC wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.

SQ Sequence 810 BP; 254 A; 177 C; 156 G; 215 T; 8 other;

Query Match 4.4%, Score 78, DB 21, Length 810;  
 Best Local Similarity 100.0%; Pred. No. 6,1e-29;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGTTCATGAGTGGTGGGCGGCTCTAGCAATAGTGGATCCCGGCGCTGACG 60



CC vivo and in vitro. It exhibits immunocontraceptive properties when  
 CC used to actively immunise male hamsters. Similarly, p34 has potential  
 CC for use in an immunocontraceptive vaccine in humans. p34  
 CC is specifically expressed in the epididymis, which supports its  
 CC potential as an immunocontraceptive target. An immunocontraceptive  
 CC vaccine may comprise antigenic fragments of p34 (AA52292, AA52293),  
 CC and an immune response should be generated against the p34 fragments  
 CC when administered to men. As the blood-testis barrier is not present in  
 CC the epididymis, the antibodies should reach the spermatozoa and  
 CC neutralise the fertilising ability of the spermatozoa, thus conferring  
 CC an immunocontraceptive protection.

XX Sequence 912 BP: 187 A: 279 C: 286 G: 160 T: 0 other:

SQ Query Match 4.3% Score 77; DB 21; Length 912;

Best Local Similarity 100.0% #Pred. No 1 oe-28;

Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGGCGCTGAGG 60  
 Db 7 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGGCGCTGAGG 66

OY 61 AATTGGCAGCAGCGCA 77

Db 67 AATTGGCAGCAGCGCA 83

#### RESULT 19

ABK43706

ID ABK43706 standard; cDNA; 1568 BP

AC ABK43706;

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PR 08-NOV-2000: 2000US-0246476.  
PR 08-NOV-2000: 2000US-0246477.  
PR 08-NOV-2000: 2000US-0246478.  
PR 08-NOV-2000: 2000US-0246523.  
PR 08-NOV-2000: 2000US-0246524.  
PR 08-NOV-2000: 2000US-0246525.  
PR 08-NOV-2000: 2000US-0246526.  
PR 08-NOV-2000: 2000US-0246527.  
PR 08-NOV-2000: 2000US-0246528.  
PR 08-NOV-2000: 2000US-0246529.  
PR 08-NOV-2000: 2000US-0246609.  
PR 08-NOV-2000: 2000US-0246610.  
PR 08-NOV-2000: 2000US-0246611.  
PR 08-NOV-2000: 2000US-0246613.  
PR 17-NOV-2000: 2000US-0249207.  
PR 17-NOV-2000: 2000US-0249208.  
PR 17-NOV-2000: 2000US-0249209.  
PR 17-NOV-2000: 2000US-0249210.  
PR 17-NOV-2000: 2000US-0249211.  
PR 17-NOV-2000: 2000US-0249212.  
PR 17-NOV-2000: 2000US-0249213.  
PR 17-NOV-2000: 2000US-0249214.  
PR 17-NOV-2000: 2000US-0249215.  
PR 17-NOV-2000: 2000US-0249216.  
PR 17-NOV-2000: 2000US-0249217.  
PR 17-NOV-2000: 2000US-0249218.  
PR 17-NOV-2000: 2000US-0249244.  
PR 17-NOV-2000: 2000US-0249245.  
PR 17-NOV-2000: 2000US-0249246.  
PR 17-NOV-2000: 2000US-0249265.  
PR 17-NOV-2000: 2000US-0249267.  
PR 17-NOV-2000: 2000US-0249299.  
PR 17-NOV-2000: 2000US-0249300.  
PR 01-DEC-2000: 2000US-0250160.  
PR 01-DEC-2000: 2000US-0250391.  
PR 05-DEC-2000: 2000US-0251030.  
PR 05-DEC-2000: 2000US-0251988.  
PR 05-DEC-2000: 2000US-0256719.  
PR 06-DEC-2000: 2000US-0256719.  
PR 06-DEC-2000: 2000US-0251479.  
PR 08-DEC-2000: 2000US-0251486.  
PR 08-DEC-2000: 2000US-0251868.  
PR 08-DEC-2000: 2000US-0251869.  
PR 08-DEC-2000: 2000US-0251989.  
PR 11-DEC-2000: 2000US-0251990.  
PR 05-JAN-2001: 2000US-0254097.  
PR 05-JAN-2001: 2000US-0259678.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Barash SC, Ruben SM;  
XX WPI: 2001-581633/65.  
XX P-PSDB: AAU87376.  
PT New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives.  
PS Claim 1: SEQ ID No 296; 837pp; English.  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
CC novel central nervous system protein. (I) and polypeptides (II) encoded  
CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes

CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
CC Query Match 4.3%; Score 77; DB 23; Length 1568;  
CC Best Local Similarity 100.0%; Pred. No. 1.9e-28;  
CC Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGACTAGTGTGATCCCCGGGCTGCAGG 60  
CC 28 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGACTAGTGTGATCCCCGGGCTGCAGG 87  
CC  
CC 61 AATTGGGACGAGCCGA 77  
CC 88 AATTCGGACGAGCCGA 104  
CC  
CC RESULT 20  
CC AAH35391  
CC ID AAH35391 standard; cDNA; 387 BP.  
CC XX AAH35391;  
CC AC AAH35391;  
CC XX 03-SEP-2001 (first entry)  
CC DT 03-SEP-2001 (first entry)  
CC XX Human colon cancer antigen encoding cDNA SEQ ID NO.2473.  
CC DE Human colon cancer: colon cancer antigen; diagnosis; detection;  
CC KW colorectal carcinoma, SS.  
CC XX Homo sapiens.  
CC OS Homo sapiens.  
CC XX WO200122220-A2.  
CC FN 05-APR-2001.  
CC PD 28-SEP-2000; 2000US-0256524.  
CC EF 29-SEP-1999; 99US-0157137.  
CC XX 03-NOV-1999; 99US-0163280.  
CC PR (HUMA-) HUMAN GENOME SCI INC.  
CC XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
CC PI WPI: 2001-235357/24.  
CC XX P-PSDB: AAG75986.  
CC PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
CC useful for preventing, diagnosing and/or treating colorectal cancers.  
CC PS Claim 1: Page 4044-4045; 9803pp; English.  
CC XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
CC the proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene  
CC therapy and vaccine production. N and P may be used in the prevention,  
CC diagnosis and treatment of diseases associated with inappropriate P  
CC expression. For example, N and P may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of P by expressing  
CC inactive proteins or to supplement the patients own production of P.  
CC Additionally, N may be used to produce the colon cancer-associated Ps.  
CC By inserting the nucleic acids into a host cell and culturing the cell  
CC to express the proteins. N and P can be used in the prevention, diagnosis



CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
CC present invention.  
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
CC missing at time of publication, meaning no sequences are present for  
CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
XX  
XX  
SQ Sequence 387 BP; 79 A, 129 C, 104 G, 70 T, 5 other;  
Query Match 4.3%; Score 76; DB 22; Length 387;  
Best Local Similarity 100.0%; Pred. No. 6.2e-28;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATGATCCCGCGGCTGCGAGG 60  
DB 35 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATGATCCCGCGGCTGCGAGG 60  
QY 61 AATTCGGCAGGAGCGG 76  
DB 95 AATTCGGCAGGAGCGG 110  
RESULT 21  
ID AAH33228 standard; cDNA; 613 BP.  
XX  
XX  
AC AAH33228;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:284.  
XX  
DE Human: colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200122920-A2  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000WO-0526524.  
XX  
PR 29-SEP-1999; 99US-0157137.  
XX  
PR 03-NOV-1999; 99US-0163280.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX  
XX WPI: 2001-235357/24.  
XX  
XX P-PSDB: AAG73797.  
XX  
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
XX useful for preventing, diagnosing and/or treating colorectal cancers -  
XX  
XX Claim 1; Page 2411; 9803pp; English.  
XX  
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
XX cancer-associated nucleic acid molecules (N) and proteins (P), where  
XX the proteins are collectively known as colon cancer antigens. The colon  
XX cancer antigens have cytostatic activity and can be used in gene  
XX therapy and vaccine production. N and P may be used in the prevention,  
XX diagnosis and treatment of diseases associated with inappropriate P  
XX expression. For example, N and P may be used to treat disorders  
XX associated with decreased expression by rectifying mutations or deletions  
XX in a patient's genome that affect the activity of P by expressing  
XX inactive proteins or to supplement the patient's own production of P.  
XX Additionally, N may be used to produce the colon cancer-associated Ps,  
XX by inserting the nucleic acids into a host cell and culturing the cell  
XX to express the proteins. N and P can be used in the prevention, diagnosis  
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
XX and AAB77789 represent sequences used in the exemplification of the

CC present invention.  
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
CC missing at time of publication, meaning no sequences are present for  
CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
XX  
XX  
SQ Sequence 613 BP; 165 A, 179 C, 151 G, 111 T, 7 other;  
Query Match 4.3%; Score 76; DB 22; Length 613;  
Best Local Similarity 100.0%; Pred. No. 6.3e-28;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATGATCCCGCGGCTGCGAGG 60  
DB 20 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTACTGATGATCCCGCGGCTGCGAGG 60  
QY 61 AATTCGGCAGGAGCGG 76  
DB 80 AATTCGGCAGGAGCGG 95  
RESULT 22  
ID ABA77069  
XX  
XX ABA77069 standard; DNA; 940 BP.  
XX  
AC ABA77069;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Proliferative glomerular nephritis-associated gene sequence SEQ ID-76  
XX  
XX kat; proliferative glomerular nephritis-associated gene; TRDH;  
KW stromal cell derived factor-2; prostacyclin-stimulation factor;  
KW TSC-22 like protein 2; kidney disease; diagnosis; kidney disorder;  
XX proliferative glomerular nephritis; ds.  
XX  
XX Rattus norvegicus.  
XX  
XX WO200173022-A1.  
XX  
XX 04-OCT-2001.  
XX  
XX 23-MAR-2001; 2001WO-JF02623.  
XX  
XX 29-MAR-2000; 2000JP-0090137.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Takeuchi K, Sekine S, Kikuchi Y, Sakurada K;  
XX  
XX WPI: 2001-616500/71.  
XX  
XX New DNA having increased expression in kidney tissues affected by  
XX proliferative glomerular nephritis for diagnosis and treatment of  
XX kidney disease and promotion of repair of damaged kidney tissue -  
XX  
XX Claim 16; Page 210-211; 314pp; Japanese.  
XX  
XX The present invention describes polynucleotide sequences of rat origin  
XX which encode proteins having increased expression in kidney tissues  
XX affected by proliferative glomerular nephritis. The proliferative  
XX glomerular nephritis-associated polynucleotide and protein sequence have  
XX nephrotropic activity. The polynucleotides can be used in the diagnosis,  
XX treatment and prevention of kidney disease, especially of proliferative  
XX glomerular nephritis, and in the repair of tissues damaged by kidney  
XX disease. ABA77002 to ABA77154 and AAG68138 to AAG68147 represent  
XX sequences given in the exemplification of the present invention.  
XX  
XX Sequence 948 BP; 257 A; 221 C; 266 G; 164 T; 32 other;  
Query Match 4.3%; Score 76; DB 22; Length 940;  
Best Local Similarity 100.0%; Pred. No. 6.3e-28;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







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PP 05-SEP-2000; 2000US-0239513
PP 06-SEP-2000; 2000US-0230437
PP 06-SEP-2000; 2000US-0230438
PP 09-SEP-2000; 2000US-0231242
PP 08-SEP-2000; 2000US-0231241
PP 08-SEP-2000; 2000US-0231241
PP 08-SEP-2000; 2000US-0231244
PP 08-SEP-2000; 2000US-0231413
PP 08-SEP-2000; 2000US-0231414
PP 08-SEP-2000; 2000US-0232080
PP 08-SEP-2000; 2000US-0232081
PP 12-SEP-2000; 2000US-0231968
PP 14-SEP-2000; 2000US-0232392
PP 14-SEP-2000; 2000US-0232398
PP 14-SEP-2000; 2000US-0232399
PP 14-SEP-2000; 2000US-0232400
PP 14-SEP-2000; 2000US-0232401
PP 14-SEP-2000; 2000US-0233063
PP 14-SEP-2000; 2000US-0233064
PP 14-SEP-2000; 2000US-0233065
PP 21-SEP-2000; 2000US-0234231
PP 21-SEP-2000; 2000US-0234231
PP 25-SEP-2000; 2000US-0234274
PP 25-SEP-2000; 2000US-0234497
PP 25-SEP-2000; 2000US-0234998
PP 26-SEP-2000; 2000US-0235484
PP 27-SEP-2000; 2000US-0235834
PP 27-SEP-2000; 2000US-0235836
PP 29-SEP-2000; 2000US-0236327
PP 29-SEP-2000; 2000US-0236367
PP 29-SEP-2000; 2000US-0236368
PP 29-SEP-2000; 2000US-0236369
PP 29-SEP-2000; 2000US-0236370
PP 02-OCT-2000; 2000US-0236802
PP 02-OCT-2000; 2000US-0237037
PP 02-OCT-2000; 2000US-0237038
PP 02-OCT-2000; 2000US-0237039
PP 02-OCT-2000; 2000US-0237040
PP 13-OCT-2000; 2000US-0239935
PP 13-OCT-2000; 2000US-0239937
PP 20-OCT-2000; 2000US-0240960
PP 20-OCT-2000; 2000US-0241231
PP 20-OCT-2000; 2000US-0241785
PP 20-OCT-2000; 2000US-0241786
PP 20-OCT-2000; 2000US-0241787
PP 20-OCT-2000; 2000US-0241808
PP 20-OCT-2000; 2000US-0241809
PP 20-OCT-2000; 2000US-0241826
PP 01-NOV-2000; 2000US-0244617
PP 08-NOV-2000; 2000US-0246474
PP 08-NOV-2000; 2000US-0246475
PP 08-NOV-2000; 2000US-0246476
PP 08-NOV-2000; 2000US-0246477
PP 08-NOV-2000; 2000US-0246478
PP 08-NOV-2000; 2000US-0246523
PP 08-NOV-2000; 2000US-0246524
PP 08-NOV-2000; 2000US-0246525
PP 08-NOV-2000; 2000US-0246526
PP 08-NOV-2000; 2000US-0246527
PP 08-NOV-2000; 2000US-0246528
PP 08-NOV-2000; 2000US-0246529
PP 08-NOV-2000; 2000US-0246532
PP 08-NOV-2000; 2000US-0246609
PP 08-NOV-2000; 2000US-0246610
PP 08-NOV-2000; 2000US-0246611
PP 08-NOV-2000; 2000US-0246613
PP 17-NOV-2000; 2000US-0249207
PP 17-NOV-2000; 2000US-0249208
PP 17-NOV-2000; 2000US-0249209
PP 17-NOV-2000; 2000US-0249210
PP 17-NOV-2000; 2000US-0249211
PP 17-NOV-2000; 2000US-0249212
PP 17-NOV-2000; 2000US-0249213
PP 17-NOV-2000; 2000US-0249214
PP 17-NOV-2000; 2000US-0249215
PP 17-NOV-2000; 2000US-0249216

PR 17-NOV-2000; 2000US-0249217
PR 17-NOV-2000; 2000US-0249218
PR 17-NOV-2000; 2000US-0249244
PR 17-NOV-2000; 2000US-0249245
PR 17-NOV-2000; 2000US-0249245
PR 17-NOV-2000; 2000US-0249265
PR 17-NOV-2000; 2000US-0249297
PR 17-NOV-2000; 2000US-0249299
PR 17-NOV-2000; 2000US-0249300
PR 01-DEC-2000; 2000US-0250160
PR 01-DEC-2000; 2000US-0250391
PR 05-DEC-2000; 2000US-0251030
PR 05-DEC-2000; 2000US-0251988
PR 05-DEC-2000; 2000US-0256719
PR 06-DEC-2000; 2000US-0251479
PR 08-DEC-2000; 2000US-0251856
PR 08-DEC-2000; 2000US-0251868
PR 08-DEC-2000; 2000US-0251869
PR 08-DEC-2000; 2000US-0251989
PR 08-DEC-2000; 2000US-0251990
PR 11-DEC-2000; 2000US-0254097
PR 05-JAN-2001; 2001US-0259678
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465460/50.
XX P-PSDB; AAU17064.
XX
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
XX prognosing disorders related to the proteins, including cancers, immune
XX disorders and neuronal disorders
XX
XX Claim 1: SEQ ID No 16; 880pp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for
XX diagnosing, preventing and treating diseases including immune system
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
XX transplant rejections and graft versus host disease, infectious diseases
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
XX other blood-related disorders (sickle cell anaemia), myeloproliferative
XX disorders, primary haematopoietic disorders, hyperproliferative
XX disorders (e.g. Gaucher's disease and cancer), neurodegenerative
XX disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
XX abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
XX disorders (e.g. glomerulonephritis), cardiovascular disorders
XX (e.g. arrhythmia), respiratory disorders, dermatological disorders,
XX wound healing, epithelial cell proliferation, endocrine disorders (e.g.
XX Addison's disease), reproductive system disorders, gastrointestinal
XX disorder (inflammatory disorders), liver disorders (cirrhosis),
XX as stimulators of B-cell responsiveness to pathogens, activators of
XX T-cells, to induce higher affinity antibodies, and as a means to induce
XX tumour proliferation in pathologies e.g. acquired immune deficiency
XX syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction
XX CC pathway protein coding sequences and PCR primers of the invention.
XX

```

Query Match 4.3%, Score 76, DB 22, Length 3789;

Best Local Similarity 100.0%, Pred. No. 6, 3e-28,

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGGAGCTCCACCGCGGTGGCGCGGCTCTAGAACTAGTGGATCCCGCGGCTCGAGG 60

25 AGCTGGAGCTCCACCGCGGTGGCGCGGCTCTAGAACTAGTGGATCCCGCGGCTCGAGG 84

Qy 61 AATTCGGACGAGCGG 76

Li 85 AATTCGGACGAGCGG 100

## RESULT 27

AAK59576  
ID AAK59576 standard; cDNA: 373 BP.  
XX AC AAK59576;  
XX DT 06-NOV-2001 (first entry)  
XX DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:4536.  
XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis, ss.  
XX OS Homo sapiens.  
PN WO200157182-A2  
XX PD 09-AUG-2001.  
XX PF 17-JAN-2001: 2001WO/US01354.  
XX 31-JAN-2000: 2000US-0179065  
PR 04-FEB-2000: 2000US-0180629  
PR 24-FEB-2000: 2000US-0184664  
PR 02-MAR-2000: 2000US-0186350  
PR 16-MAR-2000: 2000US-0193874  
PR 17-MAR-2000: 2000US-0190076  
PR 18-APR-2000: 2000US-0198129  
PR 14-MAY-2000: 2000US-0205515  
PR 28-JUN-2000: 2000US-0209467  
PR 30-JUN-2000: 2000US-0215135  
PR 07-JUL-2000: 2000US-0216647  
PR 07-JUL-2000: 2000US-0216647  
PR 11-JUL-2000: 2000US-0217487  
PR 11-JUL-2000: 2000US-0217496  
PR 14-JUL-2000: 2000US-0218290  
PR 25-JUL-2000: 2000US-0220093  
PR 26-JUL-2000: 2000US-0220964  
PR 14-AUG-2000: 2000US-0224518  
PR 14-AUG-2000: 2000US-0225213  
PR 14-AUG-2000: 2000US-0225214  
PR 14-AUG-2000: 2000US-0225246  
PR 14-AUG-2000: 2000US-0225267  
PR 14-AUG-2000: 2000US-0225268  
PR 14-AUG-2000: 2000US-0225268  
PR 14-AUG-2000: 2000US-0225447  
PR 14-AUG-2000: 2000US-0225757  
PR 14-AUG-2000: 2000US-0225758  
PR 14-AUG-2000: 2000US-0225759  
PR 18-AUG-2000: 2000US-0226279  
PR 22-AUG-2000: 2000US-0226281  
PR 22-AUG-2000: 2000US-0226468  
PR 22-AUG-2000: 2000US-0227182  
PR 23-AUG-2000: 2000US-0227609  
PR 30-AUG-2000: 2000US-0228924  
PR 01-SEP-2000: 2000US-0229287  
PR 01-SEP-2000: 2000US-0229343  
PR 01-SEP-2000: 2000US-0229344  
PR 01-SEP-2000: 2000US-0229345  
PR 05-SEP-2000: 2000US-0229504  
PR 05-SEP-2000: 2000US-0229513  
PR 06-SEP-2000: 2000US-0230437  
PR 06-SEP-2000: 2000US-0230438  
PR 08-SEP-2000: 2000US-0231242  
PR 08-SEP-2000: 2000US-0231243  
PR 08-SEP-2000: 2000US-0231244  
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PR 08-SEP-2000: 2000US-0231414  
PR 08-SEP-2000: 2000US-0231490  
PR 08-SEP-2000: 2000US-0232891  
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PR 14-SEP-2000: 2000US-0232397.  
PR 14-SEP-2000: 2000US-0232398.  
PR 14-SEP-2000: 2000US-0232399.  
PR 14-SEP-2000: 2000US-0232400.  
PR 14-SEP-2000: 2000US-0232401.  
PR 14-SEP-2000: 2000US-0233063.  
PR 14-SEP-2000: 2000US-0233064.  
PR 14-SEP-2000: 2000US-0233065.  
PR 21-SEP-2000: 2000US-0234223.  
PR 21-SEP-2000: 2000US-0234274.  
PR 25-SEP-2000: 2000US-0234997.  
PR 25-SEP-2000: 2000US-0234998.  
PR 26-SEP-2000: 2000US-0235484.  
PR 27-SEP-2000: 2000US-0235834.  
PR 27-SEP-2000: 2000US-0235836.  
PR 29-SEP-2000: 2000US-0236327.  
PR 29-SEP-2000: 2000US-0236367.  
PR 29-SEP-2000: 2000US-0236368.  
PR 29-SEP-2000: 2000US-0236369.  
PR 29-SEP-2000: 2000US-0236370.  
PR 02-OCT-2000: 2000US-0236802.  
PR 02-OCT-2000: 2000US-0237037.  
PR 02-OCT-2000: 2000US-0237038.  
PR 02-OCT-2000: 2000US-0237039.  
PR 02-OCT-2000: 2000US-0237040.  
PR 13-OCT-2000: 2000US-0239935.  
PR 13-OCT-2000: 2000US-0239937.  
PR 20-OCT-2000: 2000US-0340960.  
PR 20-OCT-2000: 2000US-0341241.  
PR 20-OCT-2000: 2000US-0341785.  
PR 20-OCT-2000: 2000US-0341786.  
PR 20-OCT-2000: 2000US-0341787.  
PR 20-OCT-2000: 2000US-0341808.  
PR 20-OCT-2000: 2000US-0341809.  
PR 20-OCT-2000: 2000US-0341826.  
PR 01-NOV-2000: 2000US-0344617.  
PR 08-NOV-2000: 2000US-0346474.  
PR 08-NOV-2000: 2000US-0346475.  
PR 08-NOV-2000: 2000US-0346476.  
PR 08-NOV-2000: 2000US-0346477.  
PR 08-NOV-2000: 2000US-0346478.  
PR 08-NOV-2000: 2000US-0346523.  
PR 08-NOV-2000: 2000US-0346524.  
PR 08-NOV-2000: 2000US-0346525.  
PR 08-NOV-2000: 2000US-0346526.  
PR 08-NOV-2000: 2000US-0346527.  
PR 08-NOV-2000: 2000US-0346528.  
PR 08-NOV-2000: 2000US-0346531.  
PR 08-NOV-2000: 2000US-0346609.  
PR 08-NOV-2000: 2000US-0346610.  
PR 08-NOV-2000: 2000US-0346611.  
PR 08-NOV-2000: 2000US-0346613.  
PR 17-NOV-2000: 2000US-0349207.  
PR 17-NOV-2000: 2000US-0349208.  
PR 17-NOV-2000: 2000US-0349209.  
PR 17-NOV-2000: 2000US-0349210.  
PR 17-NOV-2000: 2000US-0349211.  
PR 17-NOV-2000: 2000US-0349212.  
PR 17-NOV-2000: 2000US-0349213.  
PR 17-NOV-2000: 2000US-0349214.  
PR 17-NOV-2000: 2000US-0349215.  
PR 17-NOV-2000: 2000US-0349216.  
PR 17-NOV-2000: 2000US-0349217.  
PR 17-NOV-2000: 2000US-0349218.  
PR 17-NOV-2000: 2000US-0349244.  
PR 17-NOV-2000: 2000US-0349245.  
PR 17-NOV-2000: 2000US-0349264.  
PR 17-NOV-2000: 2000US-0349265.  
PR 17-NOV-2000: 2000US-0349297.  
PR 17-NOV-2000: 2000US-0349299.  
PR 17-NOV-2000: 2000US-0349300.  
PR 01-DEC-2000: 2000US-0250160.  
PR 01-DEC-2000: 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 04-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254007.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.

XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 DR WPI; 2001-483426/52.  
 DR P-PSDB; AAM86795.

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides.  
 PT useful for preventing, diagnosing and/or treating cancers and  
 PT metastasis.

XX Claim 1: SEQ ID NO 4636; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patients own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent the  
 CC diagnosis and treat metastases of hematopoietic-related diseases, especially  
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK4703  
 CC to AAK87694 represent human immune/hematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54946 and AAM2160  
 CC represent sequences used in the exemplification of the present invention.

XX SQ Sequence 373 BP; 59 A; 129 G; 109 C; 73 T; 3 other.

Query Match 4.2%; Score 75; DB 22; Length 373;  
 Best Local Similarity 100.0%; Pred No. 2e-27;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCATCGCGGTGGCGGCGCTCTAGAACTATGATCCGCGGCTGACG 59

Db 19 AGCTGGAGCTCCATCGCGGTGGCGGCGCTCTAGAACTATGATCCGCGGCTGACG 59

QY 61 AATTCGGCAGCAGGCC 75

Db 79 AATTCGGCAGCAGGCC 93

RESULT 28

AAK60386  
 ID AAK60386 standard; cDNA; 411 BP.

XX AC AAK60386;

XX DT 06-NOV-2001 (first entry)

XX Human immune/hematopoietic antigen encoding cDNA SEQ ID NO:5446

XX Human; immune; hematopoietic; immune/hematopoietic antigen; cancer;  
 KW cytotatic; gene therapy; vaccine; metastasis; ss.

XX OS Homo sapiens.

XX

PN W0200157182-A2.  
 XX 09-AUG-2001.  
 XX  
 PR 17-JAN-2001; 2001WO-US01354.  
 XX  
 PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
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 PR 14-AUG-2000; 2000US-0225266.  
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 PR 14-AUG-2000; 2000US-0225270.  
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 PR 14-AUG-2000; 2000US-0225758.  
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 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
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 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0233080.  
 PR 08-SEP-2000; 2000US-0233081.  
 PR 12-SEP-2000; 2000US-0233968.  
 PR 14-SEP-2000; 2000US-0233997.  
 PR 14-SEP-2000; 2000US-0233998.  
 PR 14-SEP-2000; 2000US-0233999.  
 PR 14-SEP-2000; 2000US-0234000.  
 PR 14-SEP-2000; 2000US-0234001.  
 PR 14-SEP-2000; 2000US-0234063.  
 PR 14-SEP-2000; 2000US-0234064.  
 PR 14-SEP-2000; 2000US-0234065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.

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PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239435.
PR 13-OCT-2000; 2000US-0239437.
PR 20-OCT-2000; 2000US-0240660.
PR 20-OCT-2000; 2000US-0241321.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249220.
PR 17-NOV-2000; 2000US-0249221.
PR 17-NOV-2000; 2000US-0249222.
PR 17-NOV-2000; 2000US-0249223.
PR 17-NOV-2000; 2000US-0249224.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250191.
PR 05-DEC-2000; 2000US-0251048.
PR 05-DEC-2000; 2000US-0251049.
PR 05-DEC-2000; 2000US-0251179.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;

XX
DE WPI: 2001-483426/52.
DE P-PSDB, AAM87605.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis.
XX
XX Claim 1. SEQ ID NO 5446, 307lpp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 411 BP, 102 A, 31 C, 83 G, 13i T, 4 other;
XX
XX Query Match 4.2%, Score 75, DB 22; Length 411;
XX Best Local Similarity 100.0%, Field No. 2e-27;
XX Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AGCTGGAGCTCCACCGCGGCGCGGCTCTAGAACTAGTGCATCCCGCGGCTGCAGG 60
Dd |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Dd 14 AGCTGGAGCTCTCACTCGCGGCGGCGGCTCTAGAACTAGTGCATCCCGCGGCTGCAGG 73
QY 61 AATTGGCGCAGCAGCC 75
Dd |||||||||||||||
Dd 74 AATTGGCGCAGCAGCC 88

RESULT 29
AAC80580
ID AAC80580 standard, cDNA; 558 BP.
XX
XX AAC80580;
XX
XX 12-FEB-2001 (first entry)
XX
XX Human secreted protein gene 50 SEQ ID NO:60.
XX
XX Human; secreted protein; immunosuppressive, antiarthritic, antirheumatic,
XX antiproliferative, cytostatic; cardiant, vasotropic; cerebroprotective;
XX neoptopic, neuroprotective, antibacterial, virucide; fungicide; cancer;
XX ophthalmological, autoimmune disease, hyperproliferative disorder,
XX cardiovascular disorder; cerebrovascular disorder; wound healing;
XX nervous system disorder; aging; chemotaxis; ss.
XX
XX Homo sapiens.
XX
XX W02000058467-A1.
XX
XX 05-OCT-2000.
XX
XX 22-MAR-2000, 2000WO-US07505.
XX
XX 26-MAR-1999; 99US-0126502.
XX 17-DEC-1999; 99US-0174110.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
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XX

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PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX WPI: 2000-611712-10  
 DR P-PSDB; AAB45169.  
 XX  
 XX Nucleic acid molecules encoding human secreted proteins, used in  
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PI Parkinson's diseases and cancers.  
 XX  
 XX Claim 4: Page 380; 440pp; English.  
 XX  
 XX Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human  
 CC secreted proteins AAB45170-B45225. Sequences AAB45170-B45225 represent  
 CC alternative polypeptides encoded by the genes, and amino acid sequences  
 CC to which they are homologous. The genes and proteins have activities  
 CC dependent on the tissues and cells in which they are expressed. Examples  
 CC of their activities include immunosuppressive; antiarthritic; vasotropic;  
 CC antirheumatic; antiproliferative; cytostatic; cardiant; antitumor;  
 CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
 CC fungicide; and ophthalmological. The secreted proteins, polypeptides,  
 CC antagonists and agonists may be useful in treating, preventing and/or  
 CC diagnosing diseases and disorders such as autoimmune diseases  
 CC e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms  
 CC of the breast or liver, cardiovascular disorders e.g. cardiac arrest,  
 CC cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous  
 CC system disorders e.g. Alzheimer's disease, infections caused by  
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.  
 CC The polypeptides can also be used to aid wound healing and epithelial  
 CC cell proliferation, to prevent skin aging due to sunburn, to maintain  
 CC organs before transplantation, for supporting cell culture of primary  
 CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can  
 CC also be used as a food additive or preservative to increase or decrease  
 CC storage capabilities. AAC80522-C80530 and AAB45119 represent sequences  
 CC used in the isolation and characterisation of the genes and proteins of  
 CC the invention.  
 XX  
 XX Sequence 558 BP; 107 A; 147 C; 169 G; 130 T; 5 other;  
 XX  
 XX Query Match 4.2%; Score 75; DB 21; Length 558;  
 XX Best Local Similarity 100.0%; Pred. No. 2e-27;  
 XX Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 QY 1 AGCTGGAGCTCCACCGCGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
 DB 54 AGCTGGAGCTCCACCGCGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 113  
 QY 61 AATTCGGCAGGAGCC 75  
 DB 114 AATTCGGCAGGAGCC 128  
 RESULT 30  
 AAA87692  
 ID AAA87692 standard; cDNA; 745 BP.  
 XX  
 XX AAA87692;  
 XX  
 XX 04-DEC-2000 (first entry)  
 XX  
 XX Human secreted protein gene 27 SEQ ID NO:37.  
 XX  
 XX Human; secreted protein; immunosuppressive, immunostimulant, neurotropic;  
 FW antiinflammatory; cardiant; vulnerary; antiulcer; anticonvulsant;  
 KW antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;  
 KW antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;  
 KW gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;  
 KW cancer; immune system disorder; hyperproliferative disorder; infection;  
 KW cardiovascular disorder; neurological disease; wound healing; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W0200043495-A2.  
 PN  
 XX

PD 27-JUL-2000.  
 XX  
 XX 18-JAN-2000, 2000WO-US00903.  
 XX  
 XX 19-JAN-1999; 99US-0116330.  
 XX  
 XX (HOMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Moore PA;  
 PI Komatsoulis G, Birse CE;  
 XX  
 XX WPI: 2000-499225/44.  
 DR P-PSDB, AAB25691.  
 XX  
 XX New isolated polynucleotide encoding a secreted protein useful for  
 PT preventing, treating or ameliorating a medical condition.  
 PI  
 XX Claim 1: Page 394; 451pp; English.  
 XX  
 XX The polynucleotide sequences given in AAA87665 to AAA87708 encodes the  
 CC human secreted proteins given in AAB25665 to AAB25755. Human secreted  
 CC proteins have activities based on the tissues and cells the genes are  
 CC expressed in. Examples of activities include: immunosuppressive;  
 CC immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer;  
 CC neurotropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;  
 CC antibacterial; antiparasitic; thrombolytic; anticoagulant;  
 CC antiarteriosclerotic and cytostatic. The secreted proteins and their  
 CC polynucleotides can be used in gene therapy and as vaccines,  
 CC chemotaxis-modulators and angiogenesis-modulators. The human secreted  
 CC proteins and polynucleotides can be used for diagnosing (the  
 CC susceptibility to) a pathological condition by determining the presence  
 CC or absence of a mutation in the polynucleotide or determining the  
 CC presence or amount of expression of the protein. The polynucleotides and  
 CC proteins can also be used in the treatment and diagnosis of cancer,  
 CC diseases of the immune system, hyperproliferative disorders,  
 CC cardiovascular disorders and neurological disease. They can also be used  
 CC to promote wound healing and to fight infection. AAA87657 to AAA87665 and  
 CC AAB25664 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 745 BP; 191 A; 214 C; 188 G; 142 T; 10 other;  
 XX  
 XX Query Match 4.2%; Score 75; DB 21; Length 745;  
 XX Best Local Similarity 100.0%; Pred. No. 2e-27;  
 XX Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 QY 1 AGCTGGAGCTCCACCGCGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
 DB 327 AGCTGGAGCTCCACCGCGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 386  
 QY 61 AATTCGGCAGGAGCC 75  
 DB 387 AATTCGGCAGGAGCC 401  
 RESULT 31  
 ABA12886  
 ID ABA12886 standard; cDNA; 829 BP.  
 XX  
 XX ABA12886;  
 XX  
 XX 23-JAN-2002 (first entry)  
 XX  
 XX Human nervous system related polynucleotide SEQ ID NO 1893.  
 XX  
 XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
 KW antiparkinsonian; antiskinning; antianaemic; antiarthritic; cancer;  
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
 KW antidiabetic; antidiabetic; antiulcer; anticonvulsant; antifungal;  
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.  
 XX  
 XX





```
XX PI Takeuchi K, Sekine S, Kikuchi Y, Sakurada K;
XX WPI: 2001-615500/71
XX New DNA having increased expression in kidney tissues affected by
XX proliferative glomerular nephritis for diagnosis and treatment of
XX kidney disease and promotion of repair of damaged kidney tissue -
XX Claim 16: Page 193-194; 314pp; Japanese.
XX The present invention describes polynucleotide sequences of rat origin
XX which encode proteins having increased expression in kidney tissues
XX affected by proliferative glomerular nephritis. The proliferative
XX glomerular nephritis-associated polynucleotide and protein sequence have
XX nephrotropic activity. The polynucleotides can be used in the diagnosis,
XX treatment and prevention of kidney disease, especially of proliferative
XX glomerular nephritis, and in the repair of tissues damaged by kidney
XX disease. ABA77002 to ABA77154 and AAC68138 to AAC68147 represent
XX sequences given in the exemplification of the present invention.
XX Sequence 954 BP; 236 A; 156 C; 136 G; 427 T; 19 other;
SQ
Query Match 4.28; Score 75; DB 22; Length 864;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGCTCTATCGGTGCGGCTCTAGAACTATGATGATGCGGCTGTCAGG 60
DB 42 AGCTGAGCTCTATCGGTGCGGCTCTAGAACTATGATGATGCGGCTGTCAGG 101
QY 61 AATTCGGCAGCAGGCC 75
DB 102 AATTCGGCAGCAGGCC 116
RESULT 34
AAC63454
ID AAC63454 standard; cDNA; 882 BP.
AC AAC63454;
XX 09-FEB-2001 (first entry)
DE Human secreted protein coding sequence SEQ ID NO: 55.
XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
XX anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder,
XX neurological disease; infection; human; secreted protein; ss.
XX Homo sapiens.
XX WO200061779-A1.
XX 19-OCT-2000
XX 06-APR-2000. 2000WO-0509068
XX 09-APR-1999; 99US-0128699.
XX 20-JAN-2000; 2000US-0177050.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM, Komatsoulis G;
XX WPI: 2000-647424/62
XX P-PSDB: AAB29846.
XX Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition -
XX PI
XX New nucleic acids and polypeptides, useful for diagnosing, preventing
```

```
PS Claim 1: Page 423; 495pp; English.
XX The invention relates to the isolation of genes AAC63410-C63458 encoding
XX 49 human secreted proteins AAB29802-E29850. The genes can be used to
XX generate fusion proteins by linking to the gene for the human
XX immunoglobulin G Fc portion (SBO101) for increasing the stability of
XX the fusion protein as compared to the human protein only. The genes and
XX proteins are useful for preventing, ameliorating or treating medical
XX conditions, e.g. by protein or gene therapy. The genes are isolated
XX from a range of human tissues disclosed in the specification. The
XX nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
XX and ovarian cancer, and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d)
XX wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.
XX Sequence 882 BP; 153 A; 277 C; 265 G; 178 T; 9 other;
SQ
Query Match 4.28; Score 75; DB 21; Length 882;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTGAGCTCTATCGGTGCGGCTCTAGAACTATGATGATGCGGCTGTCAGG 60
DB 43 AGCTGAGCTCTATCGGTGCGGCTCTAGAACTATGATGATGCGGCTGTCAGG 102
QY 61 AATTCGGCAGCAGGCC 75
DB 103 AATTCGGCAGCAGGCC 117
RESULT 35
AAS33285/C
ID AAS33285 standard; cDNA; 1243 BP.
XX AAS33285;
AC AAS33285;
XX 04-DEC-2001 (first entry)
DE DNA encoding human secreted protein, Seq ID No 244.
XX Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
XX rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular;
XX cerebroprotective; thrombolytic, antimicrobial, ophthalmological;
XX cystostatic; Alzheimer's disease, Parkinson's disease; human; cancer;
XX multiple sclerosis; cancer; hyperproliferative disorder; infection;
XX Gaucher's disease; neurological disease; cerebrovascular disorder;
XX thrombosis; wound healing; ss.
XX Homo sapiens.
XX WO200153326-A2.
XX 02-AUG-2001.
XX 17-JAN-2001, 2001WO-US01347.
XX 31-JAN-2000; 2000US-0179065.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-451931/48.
XX P-PSDB: AAU20576.
XX New nucleic acids and polypeptides, useful for diagnosing, preventing
```











PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
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 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249254.  
 PR 17-NOV-2000; 2000US-0249265.  
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 PR 17-NOV-2000; 2000US-0249269.  
 PR 17-NOV-2000; 2000US-0249400.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251048.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 06-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251858.  
 PR 08-DEC-2000; 2000US-0251859.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2000US-0259678.  
 (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-488781/43  
 P-PSDB: AAM43651

New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -

Claim 1: SEQ ID NO 165; 664pp - Sequence Listing: English.

The invention relates to human polynucleotides (AAM43651) and the encoded proteins (AAM43652) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pat\\_sequences](http://ftp.wipo.int/pub/published/pat_sequences)

Sequence 1355 BP; 283 A; 370 C; 379 G; 314 T; 9 other.

Query Match 4.2%; Score 75; DB 22; Length 1355;  
 Best Local Similarity 100.0%; Pred. No. 2e-27;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTGGAGCTCCACCGGGTGGCGGCGCTCTAGAACTAGTGGATCCCCCGGCTGCAGG 60  
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 DL 911 AGCTGGAGCTCCACCGGGTGGCGGCGCTCTAGAACTAGTGGATCCCCCGGCTGCAGG 852

OY 61 AATTCGGCAGGACC 75  
 ||||||||||||||||  
 DL 851 AATTCGGCAGGACC 837

RESULT 39

AAS31368/c

IL AAS31368 standard; cDNA; 1355 BP.

XX AC AAS31368;

XX XX 04-DEC-2001 (first entry)

XX XX Human cDNA encoding a novel extracellular matrix protein, Seq ID NO 162.  
 XX XX Human, secreted extracellular matrix protein; ss: immunomodulatory;  
 KW Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiac; vascular;  
 KW cerebroprotective, thrombolytic, antimicrobial, ophthalmic, cytostatic;  
 KW antialzheimers, immune/autoimmune disease, HIV infection, anaemia;  
 KW human immunodeficiency virus; rheumatoid arthritis, multiple sclerosis;  
 KW cancers, hyperproliferative disorder, breast neoplasm, melanoma;  
 KW Sezary syndrome; Gaucher's disease, neurological diseases;  
 KW Alzheimer's disease, Parkinson's disease, cardiovascular disorder;  
 KW cardiac arrest; tachycardia; angina; infection; corneal infections;  
 KW wound healing; immunogen, gene therapy; antisense; food additive.

OS Homo sapiens.

XX XX WO200153368-A1.

XX XX 02-AUG-2001.

XX XX 17-JAN-2001; 2001WO-US01348.

XX XX 31-JAN-2000; 2000US-0179065.

XX XX 04-FEB-2000; 2000US-0180628.

XX XX 24-FEB-2000; 2000US-0184664.

XX XX 02-MAR-2000; 2000US-0186350.

XX XX 16-MAR-2000; 2000US-0189874.

XX XX 17-MAR-2000; 2000US-0190076.

XX XX 18-APR-2000; 2000US-0198123.

XX XX 19-MAY-2000; 2000US-0205515.

XX XX 07-JUN-2000; 2000US-0209467.

XX XX 28-JUN-2000; 2000US-0214886.

XX XX 30-JUN-2000; 2000US-0215135.

XX XX 07-JUL-2000; 2000US-0216647.

XX XX 07-JUL-2000; 2000US-0216880.

XX XX 11-JUL-2000; 2000US-0217487.

XX XX 11-JUL-2000; 2000US-0217496.

XX XX 14-JUL-2000; 2000US-0218290.

XX XX 25-JUL-2000; 2000US-0220963.

XX XX 26-JUL-2000; 2000US-0220964.

XX XX 14-AUG-2000; 2000US-0224518.

XX XX 14-AUG-2000; 2000US-0224519.

XX XX 14-AUG-2000; 2000US-0225213.

XX XX 14-AUG-2000; 2000US-0225214.

XX XX 14-AUG-2000; 2000US-0225266.

XX XX 14-AUG-2000; 2000US-0225267.

XX XX 14-AUG-2000; 2000US-0225268.

XX XX 14-AUG-2000; 2000US-0225270.

XX XX 14-AUG-2000; 2000US-0225447.

XX XX 14-AUG-2000; 2000US-0225757.

XX XX 14-AUG-2000; 2000US-0225758.

XX XX 14-AUG-2000; 2000US-0225759.

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 PR 20-OCT-2000; 2000US-0241787  
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 PR 17-NOV-2000; 2000US-0249297  
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 PR 06-DEC-2000; 2000US-0251479  
 PR 08-DEC-2000; 2000US-0251856  
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 PR 08-DEC-2000; 2000US-0251869  
 PR 08-DEC-2000; 2000US-0251989  
 PR 08-DEC-2000; 2000US-0251990  
 PR 11-DEC-2000; 2000US-0254097  
 PR 05-JAN-2001; 2001US-0259678

XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI, 2001:465572/50.  
 DR F-SDDB, AAU19797.  
 XX  
 PT Nucleic acid molecules encoding human secreted extracellular matrix  
 PT proteins, used in preventing, treating or ameliorating a disorder, e.g.  
 PT Alzheimer's and Parkinson's diseases and cancers -  
 XX Claim 1, SEQ ID NO 182, 577pp, English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules encoding  
 CC novel human secreted extracellular matrix proteins (SPs). The  
 CC polynucleotides and proteins are used to prevent, treat a medical  
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. For example, disorders associated with decreased  
 CC expression of SPs. The SP polynucleotide or a vector expressing them may  
 CC be administered to treat diseases by gene therapy. Antisense molecules  
 CC may be administered to down regulate expression of SPs by binding with  
 CC the cells own genes and preventing their expression. The polynucleotides  
 CC may also be used as tRNA probes in diagnostic assays. The SPs may also be  
 CC used as antigens to produce antibodies and to identify modulators  
 CC (agonists and antagonists) of the SPs. The anti-(SP) antibodies and  
 CC SP and as diagnostic agents for detecting the presence of SPs in samples.  
 CC The disorders include for example: immune/autoimmune diseases (e.g. HIV  
 CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis  
 CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.  
 CC melanomas, neoplasms of the breast or liver, Sezary syndrome and  
 CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,  
 CC Parkinson's disease), cardiovascular/cerebrovascular disorders (e.g. cardiac  
 CC arrest, tachycardia and angina), infections caused by bacteria, viruses  
 CC and fungi and ocular disorders (e.g. corneal infections). Other uses  
 CC include wound healing, maintenance of organs before transplantation,

Query Match 4 29; Score 75; DB 22; Length 1355;  
 Best Local Similarity 100.0%; Fred. No. 2e-27;

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Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 AGCTGAGACTCAGCGGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGACG 60
    |||||||
Db 911 AGCTGAGACTCAGCGGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGACG 852
QY 61 AATTCGGCAGCAGGC 75
    |||||||
Db 851 AATTCGGCAGCAGGC 837

RESULT 40
AAS35029/G
ID AAS35029 standard; cDNA; 1355 BP.
XX
AC AAS35029;
XX
DT 04-DEC-2001 (first entry)
XX
DE cDNA encoding novel human neoplastic disease associated polypeptide #244.
XX
KW Human; neoplastic disease associated polypeptide; cancer; gene therapy.
KW hyperproliferative disorder; neural disorder; immune system disorder.
PW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
XX
OS Homo sapiens
XX
PN W0200155163-A1
XX
PD 02-AUG-2001
XX
PF 17-JAN-2001; 2001WO-060158
XX
PR 31-JAN-2000; 2000US-0179065
PR 04-FEB-2000; 2000US-0180628
PR 24-FEB-2000; 2000US-0184664
PR 02-MAR-2000; 2000US-0186350
PR 16-MAR-2000; 2000US-0188874
PR 17-MAR-2000; 2000US-0190076
PR 18-APR-2000; 2000US-0198123
PR 19-MAY-2000; 2000US-0205515
PR 07-JUN-2000; 2000US-0209457
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PR 14-AUG-2000; 2000US-0225758
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PR 17-NOV-2000; 2000US-0249212
PR 17-NOV-2000; 2000US-0249213
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PP 27-SEP-2000; 2000US-0235834.  
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 PR 29-SEP-2000; 2000US-0236327.  
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 PR 17-NOV-2000; 2000US-0249217.  
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 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
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 PR 17-NOV-2000; 2000US-0249297.  
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 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
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 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
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 PR 06-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251969.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 11-DEC-2000; 2000US-0251990.  
 PR 05-JAN-2001; 2000US-0254897.  
 PR 05-JAN-2001; 2000US-0259678.  
 XX (HUMA-) HUMAN GENOME SCI INC.

XX

Rosen CA, Barash SC, Ruben SM;

WFI: 2001-465460/50.

DR P-PSDB; AAU17387.

XX

Novel polypeptides useful for diagnosing, treating, preventing and/or  
 pronosing disorders related to the proteins, including cancers, immune  
 disorders and neuronal disorders -

Claim 1: SEQ ID No 339; 880pp; English.

XX

The invention relates to novel isolated polypeptides (I), and  
 polynucleotides (II), (I), (II) and the antibody to (I) are useful for  
 diagnosing, preventing and treating diseases including immune system  
 disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
 disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
 transplant rejections and graft versus host disease, infectious diseases  
 (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
 other blood-related disorders (sickle cell anaemia), myeloproliferative  
 disorders, primary haematopoietic disorders, hyperproliferative  
 disorders (e.g. Gaucher's disease and cancer), neurodegenerative  
 disorders (e.g. Alzheimer's disease and Parkinson's disease), chromosomal  
 abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal  
 disorders (e.g. glomerulonephritis), cardiovascular disorders  
 (e.g. arrhythmia), respiratory disorders, dermatological disorders, in  
 wound healing, epithelial cell proliferation, endocrine disorders (e.g.  
 Addison's disease), reproductive system disorders, gastrointestinal  
 disorder (inflammatory disorders), liver disorders (cirrhosis),  
 as stimulators of B-cell responsiveness to pathogens, activators of  
 T-cells, to induce higher affinity antibodies, and as a means to induce  
 tumour proliferation in pathologies e.g. acquired immune deficiency  
 syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction  
 pathway protein coding sequences and PCR primers of the invention.

XX

Query Match 4.2%, Score 75, DB 22; Length 1744;

Best Local Similarity 100.0%, Pred. No. 2e-27;

Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGTCGAGG 60

|||||

Db 46 ACCTGGAGCTCCACCGCGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGTCGAGG 105

|||||

QY 61 AATTCGGCAGGACC 75

|||||

Db 106 AATTCGGCAGGACC 120

RESULT 45

AAZ48809  
IC AAZ48809 standard; cDNA, 1802 BP.

XX

AC AAZ48809;

XX

DT 21-MAR-2000 (first entry)

XX

DE Soybean inositol 1,3,4-triphosphate 5/6-kinase coding sequence.

XX

KW Inositol 1,3,4-triphosphate 5/6-kinase; phytic acid, genetic mapping;  
 myo-inositol 1,2,3,4,5,6-hexaphosphate; biosynthetic enzyme; phytate;  
 animal feed; ss.

XX

OS Glycine max.

XX

FN WC975679-A1.

XX

PD 04-NOV-1999.

XX

FF 22-APR-1999; 99WO-US08790.

XX

PR 24-APR-1998; 98US-0082960.

XX



PA (DUPO ) DU PONT DE NEMOURS & CO E. I.  
 XX Cahoon RE, Carlson TJ, Hitz WD, Pearlstein RW;  
 PI WPI: 2000-072179/06.  
 DR P-PSDB: AAV59425.  
 XX  
 PT Novel phytic acid biosynthetic enzymes used to alter the level of the  
 PT enzyme in transgenic plants.  
 XX  
 PS Claim 2: Page 49: 63pp: English  
 XX  
 XX This sequence encodes an inositol 1,3,4-triphosphate 5-phosphatase (ITK)  
 CC protein of the invention. ITK is a phytic acid (Myo-inositol  
 CC 1,2,3,4,5,6-hexaphosphate) biosynthetic enzyme. The ITK enzymes of the  
 CC invention may be prepared recombinantly and used to raise antibodies,  
 CC which are used for detecting the enzymes *in situ* in cells or *in vitro*  
 CC in cell extracts. The polynucleotides of the invention may be used to  
 CC create transgenic plants in which the ITK levels are present at higher  
 CC or lower levels than normal, or in cell types or developmental processes  
 CC where they are not normally found. This would alter the level of  
 CC 1,3,4-triphosphate 5/6 Kinase found in those cells. In addition, it may  
 CC be desirable to eliminate expression of ITK genes for certain  
 CC applications. The polynucleotides also serve as a source of probes and  
 CC primers, which are useful for genetic mapping, as markers for traits  
 CC linked to those genes, and to isolate homologous sequences from other  
 CC species, as well as for physical mapping. Decreased amounts of phytate  
 CC and increased amounts of available phosphate in animal feeds such as corn  
 CC would lead to improved feed efficiency. The proteins of the present  
 CC invention lead to a better understanding of the phytic acid biosynthesis  
 CC pathway, allowing it to be exploited for commercial uses, e.g. in animal  
 CC feeds.  
 XX  
 SQ Sequence 1802 BP: 419 A; 509 C; 443 G; 431 T; 0 other;  
 Query Match 4.2%; Score 75; DB 21; Length 1802;  
 Best Local Similarity 100.0%; Prod. No. 2e-27;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTGAGCTCCACCGGCTGGGCGGCTTTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
 DB 170 AGCTGAGCTCCACCGGCTGGGCGGCTTTAGAACTAGTGGATCCCGCGGCTGCAGG 249  
 QY 61 AATTCGGCAGCAGCC 75  
 DB 230 AATTCGGCAGCAGCC 244  
 RESULT 46  
 ID ABL92356  
 XX ABL92356 standard; cDNA; 2005 BP.  
 AC ABL92356;  
 XX  
 XX 06-JUN-2002 (first entry)  
 DE Human secreted protein coding sequence SEQ ID NO: 22.  
 XX  
 XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW radiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200216389-A1  
 PN  
 XX 28-FEB-2002.  
 PD  
 XX 17-JAN-2001; 2001WO-US01347.  
 PF  
 XX 18-AUG-2000; 2000US-226291P  
 PR

XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
 PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
 PI Ni J;  
 XX WPI: 2002-292054/23.  
 DR P-PSDB: ABB94028.  
 XX  
 XX Isolated nucleic acids encoding 23 secreted proteins useful for the  
 PT diagnosis and treatment of e.g. cancer, HIV infection, stroke and  
 PT Rheumatoid arthritis.  
 XX  
 XX Claim 1: Page 435-436; 517pp: English.  
 XX  
 XX The invention relates to the isolation of genes ABL92336-92393 encoding  
 CC 79 human secreted proteins by linking to the gene for the human  
 CC generate fusion proteins (SEQID1) for increasing the stability of  
 CC immunoglobulin G Fc portion (SEQID2) to the human protein only. The genes and  
 CC the fusion protein as compared to the human protein only. The genes and  
 CC proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated  
 CC from a range of human tissues disclosed in the specification. The  
 CC nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
 CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound  
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
 CC and (f) infectious diseases such as viral, bacterial, fungal and  
 CC parasitic infections.  
 XX  
 SQ Sequence 2005 BP, 423 A, 422 C, 467 G, 614 T; 9 other;  
 Query Match 4.2%; Score 75; DB 24; Length 2005;  
 Best Local Similarity 100.0%; Prod. No. 2e-27;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTGAGCTCCACCGGCTGGGCGGCTTTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
 DB 37 AGCTGAGCTCCACCGGCTGGGCGGCTTTAGAACTAGTGGATCCCGCGGCTGCAGG 96  
 QY 61 AATTCGGCAGCAGCC 75  
 DB 97 AATTCGGCAGCAGCC 111  
 RESULT 47  
 ID AAL02661  
 XX AAL02661 standard; cDNA; 2099 BP.  
 AC AAL02661;  
 XX  
 XX 21-NOV-2001 (first entry)  
 DE Human reproductive system related antigen cDNA SEQ ID NO: 2662.  
 XX Human reproductive system related antigen; reproductive system disorder;  
 KW cancer; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200155320-A2.  
 PN  
 XX 02 AUG-2001.  
 PD  
 XX 17-JAN-2001; 2001WO-US01349.  
 PF  
 XX 21-JAN-2000; 2000US-0174065.  
 PR

PP 04-FEB-2000; 2000US-0180628  
PP 24-FEB-2000; 2000US-0184564  
PP 02-MAR-2000; 2000US-0186360  
PP 16-MAR-2000; 2000US-0189874  
PP 17-MAR-2000; 2000US-0190076  
PP 18-APR-2000; 2000US-0198123  
PP 19-MAY-2000; 2000US-0205515  
PP 07-JUN-2000; 2000US-0209457  
PP 28-JUN-2000; 2000US-0214886  
PP 30-JUN-2000; 2000US-0215135  
PP 07-JUL-2000; 2000US-0216647  
PP 07-JUL-2000; 2000US-0216680  
PP 11-JUL-2000; 2000US-0217487  
PP 11-JUL-2000; 2000US-0217496  
PP 14-JUL-2000; 2000US-0218290  
PP 26-JUL-2000; 2000US-0220963  
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PP 18-AUG-2000; 2000US-0225759  
PP 22-AUG-2000; 2000US-0226681  
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PP 22-AUG-2000; 2000US-0227182  
PP 23-AUG-2000; 2000US-0227009  
PP 30-AUG-2000; 2000US-0228024  
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PP 01-SEP-2000; 2000US-0229344  
PP 01-SEP-2000; 2000US-0229345  
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PP 01-DEC-2000; 2000US-0250391  
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PP 05-DEC-2000; 2000US-0251988  
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PP 05-DEC-2000; 2000US-0256719  
PP 05-DEC-2000; 2000US-0256719  
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PP 08-DEC-2000; 2000US-0251869  
PP 08-DEC-2000; 2000US-0251989  
PP 08-DEC-2000; 2000US-0251990  
PP 11-DEC-2000; 2000US-0254097  
PP 01-JAN-2001; 2000US-0254678

(HUMA-) HUMAN GENOME SCI INC.

Pasen CA, Barash SC, Puben SM;

WFI, 2001-465570/50.

Isolated nucleic acid molecule encoding a reproductive system antigen -  
is used in preventing, treating or ameliorating a medical condition -  
Disclosure, SEQ ID NO 2662, 1297pp + Sequence Listing, English.



08-NOV-2000: 2000US-0246610.  
 08-NOV-2000: 2000US-0246611.  
 08-NOV-2000: 2000US-0246613.  
 17-NOV-2000: 2000US-0249207.  
 17-NOV-2000: 2000US-0249208.  
 17-NOV-2000: 2000US-0249209.  
 17-NOV-2000: 2000US-0249210.  
 17-NOV-2000: 2000US-0249211.  
 17-NOV-2000: 2000US-0249212.  
 17-NOV-2000: 2000US-0249213.  
 17-NOV-2000: 2000US-0249214.  
 17-NOV-2000: 2000US-0249215.  
 17-NOV-2000: 2000US-0249216.  
 17-NOV-2000: 2000US-0249217.  
 17-NOV-2000: 2000US-0249218.  
 17-NOV-2000: 2000US-0249244.  
 17-NOV-2000: 2000US-0249245.  
 17-NOV-2000: 2000US-0249284.  
 17-NOV-2000: 2000US-0249285.  
 17-NOV-2000: 2000US-0249287.  
 17-NOV-2000: 2000US-0249299.  
 17-NOV-2000: 2000US-0249300.  
 01-DEC-2000: 2000US-0250160.  
 01-DEC-2000: 2000US-0250391.  
 05-DEC-2000: 2000US-0251040.  
 05-DEC-2000: 2000US-0251048.  
 05-DEC-2000: 2000US-0256719.  
 06-DEC-2000: 2000US-0251479.  
 08-DEC-2000: 2000US-0251856.  
 08-DEC-2000: 2000US-0251868.  
 08-DEC-2000: 2000US-0251869.  
 08-DEC-2000: 2000US-0251889.  
 08-DEC-2000: 2000US-0251990.  
 11-DEC-2000: 2000US-0254007.  
 05-JAN-2001: 2000US-0259678.  
 (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-483232/52.

Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.

Claim 1: SEQ ID NO 990, 766pp, English.

The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a cDNA of the invention.

Sequence 2099 BP; 499 A; 587 C; 516 G; 487 T; 10 other;

Query Match 4.2%; Score 75; DB 23; Length 2099;  
 Best Local Similarity 100.0%; Pred. No. 2e-27;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTGGATCCCGGCTTCAAG 46  
 DB 393 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTGGATCCCGGCTTCAAG 452  
 QY 61 AATTGGGACAGGAGC 75  
 DB 453 AATTGGGACAGGAGC 467

RESULT 49  
 AAH35162  
 ID AAH35162 standard; cDNA; 200 BP.

XX AAH35162;  
 03-SEP-2001 (first entry)  
 Human colon cancer antigen encoding cDNA SEQ ID NO:2244.  
 Human, colon cancer, colon cancer antigen, diagnosis; detection;  
 colorectal carcinoma; ss.  
 Homo sapiens.  
 W020012920-A2.  
 05-APR-2001.  
 28-SEP-2000: 2000WO-US26524.  
 29-SEP-1999: 99US-0157137.  
 03-NOV-1999: 99US-0163280.  
 (HUMA-) HUMAN GENOME SCI INC.  
 Ruben SM, Barash SC, Birse CE, Rosen CA;  
 WPI: 2001-235357/24.  
 P-PSDB; AAG75757.  
 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

Claim 1, Page 3747, 9803pp, English.

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAH77789 represent sequences used in the exemplification of the present invention. R.N. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.

Sequence 200 BP; 40 A; 62 C; 57 G; 31 T; 10 other;

Query Match 4.2%; Score 74; DB 22; Length 200;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-27;  
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTGGATCCCGGCTTCAAG 60  
 DB 47 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTGGATCCCGGCTTCAAG 106  
 QY 61 AATTGGGACAGGAGC 74  
 DB 107 AATTGGGACAGGAGC 120

RESULT 50  
 AAH35170  
 ID AAH35170 standard; cDNA; 247 BP.  
 XX  
 AC AAH35170;

XX 03-SEP-2001 (first entry)  
 XX Human colon cancer antigen encoding cDNA SEQ ID NO:2252.  
 XX Human: colon cancer; colon cancer antigen; diagnosis: detection;  
 KW colorectal carcinoma; ss.  
 XX Homo sapiens.  
 XX WO200122920-A2.  
 XX 05-APR-2001.  
 XX 28-SEP-2000: 2000WO-US26524.  
 XX 29-SEP-1999: 99US-0157137.  
 XX 03-NOV-1999: 99US-0163280.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
 WI: 2001-235357/24.  
 P-PSDB: AAG75765.  
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX Claim 1: Page 3756; 9803pp; English.  
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 cancer-associated nucleic acid molecules (N) and proteins (P), where  
 the proteins are collectively known as colon cancer antigens. The colon  
 cancer antigens have cytostatic activity and can be used in gene  
 therapy and vaccine production. N and P may be used in the prevention,  
 diagnosis and treatment of diseases associated with inappropriate p  
 expression. For example, N and P may be used to treat disorders  
 associated with decreased expression by rectifying mutations or deletions  
 in a patient's genome that affect the activity of P by expressing  
 inactive proteins or to supplement the patient's own production of P.  
 Additionally, N may be used to produce the colon cancer-associated Ps,  
 by inserting the nucleic acids into a host cell and culturing the cell  
 to express the proteins. N and P can be used in the prevention, diagnosis  
 and treatment of colorectal carcinomas and cancers. AAH37195 to AAH37204  
 and AAG77789 represent sequences used in the exemplification of the  
 present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX Sequence 247 BP, 57 A, 66 C, 69 G, 50 T, 5 other,

Query Match 4.28; Score 74; DB 22; Length 247;  
 Best Local Similarity 100.0%; Pred. No 6.4e-27;  
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 63 AATCGGAGTCTATCTGGGAGTGGGGGCTGATGAACTAGTGGATATCTGGGAGTGGGAGG 122  
 (|||||)|||||  
 QY 61 AATTCGGCAGCAGC 74  
 (|||||)|||||  
 DB 123 AATTCGGCAGCAGC 136  
 (|||||)|||||

Search completed: October 31, 2002, 10:16:36  
 Job time : 298 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 11:13.10 , Search time 63 Seconds  
(without alignments)  
9381 217 Million cell updates/sec

Title: us-09-854-300-7  
Perfect score: 1774  
Sequence: 1 agctgagctccaccgcggt. .... ataggcaagttctctctcag 1774

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 310279 seqs, 166577418 residues

Word size : 0

Total number of hits satisfying chosen parameters: 620558

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

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2: /cgn2\_6/ptodata/1/pubna/PT\_NEW\_PUB.seq.\*  
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12: /cgn2\_6/ptodata/1/pubna/us10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubna/us06\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubna/us06\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	824	46.4	2306	10	US-09-764-864-43
2	704	39.7	1250	10	US-09-764-864-519
3	275	15.5	643	9	US-10-046-935-1815
4	186	10.5	340	10	US-09-783-590-3523
5	167	9.4	435	10	US-09-920-300A-1176
6	167	9.4	435	12	US-10-033-528-1176
7	80	4.5	922	10	US-09-800-729-23
8	76	4.3	1772	10	US-09-764-870-192
9	75	4.2	1355	10	US-09-764-853-148
10	74	4.2	496	10	US-09-764-853-404
11	74	4.2	640	10	US-09-908-711-28
12	74	4.2	737	10	US-09-764-853-172
13	74	4.2	791	10	US-09-764-853-305
14	74	4.2	796	10	US-09-764-853-365
15	74	4.2	852	10	US-09-764-853-50
16	74	4.2	852	10	US-09-764-853-50
17	74	4.2	1190	10	US-09-764-898-123
18	74	4.2	1190	10	US-09-410-194-14
19	74	4.2	1454	10	US-09-764-864-9

20	74	4.2	1707	10	US-09-764-870-217	Sequence 217, App
21	74	4.2	1788	10	US-09-764-898-40	Sequence 40, Appl
22	74	4.2	2005	10	US-09-764-903-22	Sequence 22, Appl
23	74	4.2	2458	10	US-09-764-864-78	Sequence 78, Appl
24	73	4.1	367	10	US-09-764-860-248	Sequence 248, Appl
25	73	4.1	421	10	US-09-764-855-67	Sequence 67, Appl
26	73	4.1	604	10	US-09-925-301-619	Sequence 619, App
27	73	4.1	618	10	US-09-764-853-136	Sequence 136, App
28	73	4.1	618	10	US-09-764-853-377	Sequence 377, App
29	73	4.1	618	10	US-09-764-898-126	Sequence 126, App
30	73	4.1	631	10	US-09-908-711-29	Sequence 29, Appl
31	73	4.1	647	10	US-09-764-898-84	Sequence 84, Appl
32	73	4.1	771	10	US-09-764-887-129	Sequence 129, App
33	73	4.1	869	10	US-09-764-864-289	Sequence 289, App
34	73	4.1	975	10	US-09-789-561-58	Sequence 58, Appl
35	73	4.1	1066	10	US-09-764-898-54	Sequence 54, Appl
36	73	4.1	1427	10	US-09-925-300-639	Sequence 639, App
37	73	4.1	1511	10	US-09-764-853-308	Sequence 308, App
38	73	4.1	1517	10	US-09-739-254-64	Sequence 64, Appl
39	73	4.1	1517	10	US-09-904-615-64	Sequence 64, Appl
40	73	4.1	1585	10	US-09-874-923-54	Sequence 54, Appl
41	73	4.1	1637	10	US-09-925-300-770	Sequence 770, App
42	73	4.1	1737	10	US-09-862-027-13	Sequence 13, Appl
43	73	4.1	1906	10	US-09-739-254-32	Sequence 32, Appl
44	73	4.1	1906	10	US-09-904-615-32	Sequence 32, Appl
45	73	4.1	2163	10	US-09-789-561-53	Sequence 53, Appl
46	73	4.1	2244	10	US-09-764-870-222	Sequence 222, App
47	73	4.1	2330	10	US-09-764-853-189	Sequence 189, App
48	73	4.1	2596	10	US-09-764-853-380	Sequence 380, App
49	73	4.1	2596	10	US-09-764-898-128	Sequence 128, App
50	73	4.1	2751	10	US-09-789-561-64	Sequence 64, Appl
51	73	4.1	2787	10	US-09-764-864-412	Sequence 412, App
52	73	4.1	2919	10	US-09-764-870-94	Sequence 94, Appl
53	73	4.1	3328	10	US-09-838-539-1	Sequence 1, Appl
54	72	4.1	439	10	US-09-925-299-484	Sequence 484, App
55	71	4.0	2045	10	US-09-861-270-1	Sequence 1, Appl
56	70	3.9	570	10	US-09-734-017A-7	Sequence 7, Appl
57	68	3.8	835	10	US-09-764-864-245	Sequence 245, App
58	68	3.8	1169	10	US-09-899-845-1	Sequence 1, Appl
59	66	3.7	344	10	US-09-924-035A-864	Sequence 864, App
60	66	3.7	752	10	US-09-956-004-108	Sequence 108, App
61	66	3.7	1712	10	US-09-925-300-643	Sequence 643, App
62	65	3.7	328	10	US-09-925-400-574	Sequence 574, App
63	65	3.7	503	10	US-09-764-847-380	Sequence 380, App
64	65	3.7	799	10	US-09-911-826A-3	Sequence 3, Appl
65	65	3.7	836	10	US-09-764-853-393	Sequence 393, App
66	65	3.7	1409	10	US-09-925-301-176	Sequence 176, App
67	65	3.7	1753	10	US-09-764-864-774	Sequence 774, App
68	65	3.7	2082	9	US-09-990-046-9	Sequence 9, Appl
69	65	3.7	2554	10	US-09-764-864-352	Sequence 352, App
70	65	3.7	3348	10	US-09-954-456-90	Sequence 90, Appl
71	65	3.7	3348	10	US-09-954-456-727	Sequence 727, App
72	64	3.6	726	10	US-09-954-456-727	Sequence 201, Appl
73	63	3.6	100	10	US-09-840-728A-19	Sequence 19, Appl
74	63	3.6	624	10	US-09-834-975-469	Sequence 469, App
75	63	3.6	1175	10	US-09-925-300-286	Sequence 286, App

## ALIGNMENTS

RESULT 1  
US-09-764-864-43  
Sequence 63, Application US/09764864  
Patent No. US20001012753A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PT23  
CURRENT APPLICATION NUMBER: US/09/764,864  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 1792

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 2306
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-63

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Query Match		46.4%	Score 824	DB 10	Length 2306
Best Local Similarity		99.6%	Pr-d	No. 0	
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QY	547	CTTTAACTGGGAAAGAAATTTACGGSTGGTAACTGTTTGGGSAAGGACATCTGAAATATC	K06		
DB	12	CTGTAACTGGGACATAGAAATTTACGGSTGGTAACTGTTTGGGSAAGGACATCTGAAATATC	71		
QY	607	TTGGTTGGGGGCTTATTAAGAAAGGGGGGGGCTGTGAACTTTGTAAGAAAGATTTATCTGGC	665		
DB	72	TTGGTTGGGGGCTTATTAAGAAAGGGGGGGCTGTGAACTTTGTAAGAAAGATTTATCTGGC	131		
QY	667	TTATGAGAGATGGGGGCTGTGGAGCGGTCATCTTTTAACTTCCCGGGTAACTGGTAATGAGT	726		
DB	132	TTATGAGAGAGGGGGCTGTGGAGCGGTCATCTTTTAACTTCCCGGGTAACTGGTAATGAGT	141		
QY	727	CATCCCCATGTCTCACCGGGTGAGTAGACATTTGTGCAATCATGATGGCAATCTGAA	786		
DB	192	CATCCCCATGTCTCACCGGGTGAGTAGATTTGTGCAATCATGATGGCAATCTGAA	251		
QY	787	AGCCACAAAAATCTGCAATCTATTCAAGAGGCTATCAAGCTGACAAATGCTATAGAAAT	846		
DB	252	AGCCACAAAAATCTGCAATCTATTCAAGAGGCTATCAAGCTGACAAATGCTATAGAAAT	311		
QY	847	AGGSAAAAAACATGGTCTTGGTAACTCACTATTTAACTTTTCTTTTGGTGGTCTCTCT	905		
DB	312	AGGSAAAAAACATGGTCTTGGTAACTCACTATTTAACTTTTCTTTTGGTGGTCTCTCT	371		
QY	906	TTTTTTATTATACGGGGTAACTTGGGCTATTTTATCTTTTATCTGGTGGTGGTGGT	965		
DB	372	TTTTTTATTATACGGGGTAACTTGGGCTATTTTATCTTTTATCTGGTGGTGGTGGT	431		
QY	966	GGAAATCAAGCTTAAAGTGGGAGGAGAGGTAATTAAGAGTAGATCTTAAGAAAGCTA	1025		
DB	432	GGAAATCAAGCTTAAAGTGGGAGGAGAGGTAATTAAGAGTAGATCTTAAGAAAGCTA	491		
QY	1026	TTGGAAATCTTAACTAGTAACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1085		
DB	492	TTGGAAATCTTAACTAGTAACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	551		
QY	1086	ATAGTTGTCTGTGGCATTCGAATGTATAAGCAATGATTTGGTACGATCTTAACT	1145		
DB	552	ATAGTTGTCTGTGGCATTCGAATGTATAAGCAATGATTTGGTACGATCTTAACT	611		
QY	1146	GCAACATATTTCCATCAAGACATGTGTGATGATGATGATGATGATGATGATGATGAT	1205		
DB	612	GCAACATATTTCCATCAAGACATGTGTGATGATGATGATGATGATGATGATGATGAT	671		
QY	1206	CTATGTGAAATGTAATATTAAGATTTTGGGAATTAAGATTTTAAATTAAGATTAAG	1265		
DB	672	CCATGTGAAATGTAATATTAAGATTTTGGGAATTAAGATTTTAAATTAAGATTAAG	731		
QY	1266	CATCTTTTAAATTCCTCTATCCATTAATTAATTAATTAATTAATTAATTAATTAAT	1325		
DB	732	CATCTTTTAAATTCCTCTATCCATTAATTAATTAATTAATTAATTAATTAATTAAT	791		
QY	1326	AGGTAATGAG	1385		
DB	792	AGGTAATGAG	851		
QY	1386	GGGCTTGGAGGAG	1445		
DB	852	GGGCTTGGAGGAG	911		
QY	1446	CAAAATCTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1505		

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RESULT 2
US-09-764-864-519
: Sequence 519, Application US/09764864
: Patent No. US20020132753A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P7223
: CURRENT APPLICATION NUMBER: US/09/764,864
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 1792
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 519
: LENGTH: 1250
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (540)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (1242)
: OTHER INFORMATION: n equals a,t,g, or c
: US-09-764-864-519

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DB	18	CTGTAAACGGCACAGAAATTTACGCTGGGCCACCGGTTTGGGCAAGCACCGGTGCAAGTCTC	77	
QY	607	TTGGTGTGGGCTTCATCCAAAGAGGGGGGGGCTGTACCTTTGGACACAAGATGCCATCTGGC	666	
DB	74	TTGGTGTGGGCTTCATCCAAAGAGGGGGGGGCTGTACCTTTGGACACAAGATGCCATCTGGC	137	
QY	667	TTATSGAGACATGGGCTGTGGAGGGGTGCATCTTTAACTTTGGCGGACCCCAATGAGGT	726	
DB	148	TTATSGAGAGGGGGGTGTGGAGGGGTGCATCTTTAACTTTGGCGGAGGCAATGAGGT	197	
QY	727	CATGCGGCGATGTCTTACGCGGGGTGGACATGATGTGTCAATCATGTGCGGCATCTCGAA	786	
DB	198	CATGCGGCGATGTCTTACGCGGGGTGGACATGATGTGTCAATCATGTGCGGCATCTCGAA	257	
QY	787	AGGCAACAAAATTTGTCAATTTATTCAAGAGGGCATACAAAGTGAACAAAGGTCATAGAAGT	846	
DB	258	AGGCAACAAAATTTGTCAATTTATTCAAGAGGGCATACAAAGTGAACAAAGTGTATAGAAGT	317	
QY	847	AGGCAAAAAACATGCGGCTTGGGTGAATCACTATTCAAATTTTCTGTCTGTCTCT	905	
DB	318	AGGCAAAAAACATGCGGCTTGGGTGAATCACTATTCAATTTTCTGTCTGTCTCTCT	377	

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QY 906 TTTTATTATTACGGCGCACTGTGGGCTATTTTATCTTTTATCTGTCGAAGCTAC 965
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QY 966 GGAATGCAAGCTCAAGCAGGAGCAGAGGCAATTAAGGCGAGATGCTAAAGAGCTA 1025
Db 438 GGAATGCAAGCTCAAGCAGGAGCAGAGGCAATTAAGGCGAGATGCTAAAGAGCTA 497
QY 1026 TTGAAGGCTTCAACTACGACACTGAACACAGGAGAGAGG-AAAATGGGCTGATGA 1084
Db 498 TTGAAGGCTTCAACTACGACACTGAACACAGGAGAGAGG-AAAATGGGCTGATGA 557
QY 1085 GATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
Db 558 GATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 617
QY 1145 TGCACCATATTTTCCATAAGACATGTTGACCCCATGGGTGTAAACACAGAGCTGC 1204
Db 618 TGCACCATATTTTCCATAAGACATGTTGACCCCATGGGTGTAAACACAGAGCTGC 677
QY 1205 CCCATGTGCTAAATGTGACATATCTAAAGCTTTGGGAATTCAGGAGAGATGGA 1264
Db 678 CCCATGTGCTAAATGTGACATATCTAAAGCTTTGGGAATTCAGGAGAGATGGA 737
QY 1265 TCAGTGTCTTACAGTCCCTGTATCCAATGAATATCTAATAGTGCCTCCCTCCCATGAA 1324
Db 738 TCAGTGTCTTACAGTCCCTGTATCCAATGAATATCTAATAGTGCCTCCCTCCCATGAA 797
QY 1325 GAGGATAATCTGATGAGATGCTATCTATGATATCTGATGATGATGATGATGATGAT 1384
Db 798 GAGGATAATCTGATGAGATGCTATCTATGATATCTGATGATGATGATGATGATGAT 857
QY 1385 CCGCTCTGGAGGAGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1444
Db 858 CCGCTCTGGAGGAGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 917
QY 1445 GCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1504
Db 918 GCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 977
QY 1505 GAACTCTTAATCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1564
Db 978 GAACTCTTAATCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027
QY 1565 AAACTTGACGCTTATATATACAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1624
Db 1038 AAACTTGACGCTTATATATACAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1097
QY 1625 TTGATAAAATTAATAAAGAGTGATATGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1684
Db 1098 TTGATAAAATTAATAAAGAGTGATATGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147
QY 1685 TATAGTTAAA 1694
Db 1158 TATAGTTAAA 1167

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RESULT 3
US-10-046-935-1815
; Sequence 1815, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046.935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2229

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1815
; LENGTH: 643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 584
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1815

Query Match 15.5%; Score 275; DB 9; Length 643;
Best Local Similarity 99.7%; Pred No 3 Ke-132;
Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1369 ACAGGGAACAGATGAACCGGCTCTGGAGGAACAGTGGCAAGTCAACAAATGAAGTCTACA 1428
Db 1 ACAGGGAACAGATGAACCGGCTCTGGAGGAACAGTGGCAAGTCAACAAATGAAGTCTACA 60
QY 1429 GCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCCTCATGTGACAAACC 1488
Db 61 GCTGGTAAACCATGAAGCAAAATCTCTGGCAGTGGATGTTATTCCTCATGTGACAAACC 120
QY 1489 AACCTTTGAAGAGAGAGAACTCCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 1548
Db 121 AACCTTTGAAGAGAGAGAACTCCTTAATCAAGAGACTGCTGTTCGAGAAATTAATCTTA 180
QY 1549 AAATCTGTATAATAGAAAACCTTGAACCAATAGTAATAACAGAACTGCCAATCAGGGCT 1608
Db 181 AAATCTGTATAATAGAAAACCTTGAACCAATAGTAATAACAGAACTGCCAATCAGGGCT 240
QY 1609 AGTTTCTATTATAATTTGGATAAAATTTAATAAATAAGAGTGATGACTGAAAGTGTCTAG 1668
Db 241 AGTTTCTATTATAATTTGGATAAAATTTAATAAATAAGAGTGATGACTGAAAGTGTCTAG 300
QY 1669 ATGACTAATATTATGCTATAGTTAAA 1694
Db 301 ATGACTAATATTATGCTATAGTTAAA 326

RESULT 4
US-09-783-590-3523
; Sequence 3523, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Posen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: po-16 2c1
; CURRENT APPLICATION NUMBER: US/09/783.590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420.856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346.731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3523
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (205)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (229)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (221)

```



OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (244)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (265)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (294)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (318)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (326)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (332)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (333)  
 OTHER INFORMATION: n equals a,t,g, or c  
 US-09-783-590-3523

Query Match 10.5% Score 186; DB 10; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-86;  
 Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 GCAATGTGACATCTCAAGCTTTGGGAATTTGGATGTTGAGATGGAATCACTGT 1271  
 DB 10 GCAATGTGACATCTCAAGCTTTGGGAATTTGGATGTTGAGATGGAATCACTGT 69  
 QY 1272 CTTTACAGTCCCTGTATCCCAATCAATATCTTAATAGTCCCTCTCCCAAGAGAGATA 1331  
 DB 70 CTTTACAGTCCCTGTATCCCAATCAATATCTTAATAGTCCCTCTCCCAAGAGAGATA 129  
 QY 1332 ATCCGAGGACGACGATCATCTGATATGCTTCAGTACAGGAGACAGATCAACCGCTC 1391  
 DB 130 ATCCGAGGACGACGATCATCTGATATGCTTCAGTACAGGAGACAGATCAACCGCTC 189  
 QY 1392 TGGAGG 1397  
 DB 190 TGGAGG 195

RESULT 5  
 US-09-920-300A-1176/c  
 Sequence 1176, Application US/09920300A  
 Patent No. US20020136728A1  
 GENERAL INFORMATION:  
 APPLICANT: King, Gordon E.  
 APPLICANT: Meagher, Madeleine Joy  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Secrist, Heather  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 FILE REFERENCE: 210121.547  
 CURRENT APPLICATION NUMBER: US/09/920.300A  
 NUMBER OF SEQ ID NOS: 1789  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1176  
 LENGTH: 435  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-920-300A-1176

Query Match 9.4% Score 167; DB 10; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-76;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 TGTTCCGAGAAATTAATCTTAAATCTGTCTAAATAGAACTTGAACCATTAAGTAA 1587  
 DB 1528 TGTTCCGAGAAATTAATCTTAAATCTGTCTAAATAGAACTTGAACCATTAAGTAA 1587

DB 337 TGTTCCGAGAAATTAATCTTAAATCTGTCTAAATAGAACTTGAACCATTAAGTAA 278  
 QY 1588 CAGAACTGCCAATCAGGGCCTAGTTCTTATTAATAATTTGAATAAATAAG 1647  
 DB 277 CAGAACTGCCAATCAGGGCCTAGTTCTTATTAATAATTTGAATAAATAAG 218  
 QY 1648 AGTGATCTACTGAAAGTGTCTCAGATGACTAATATTATGCTATAGTTAA 1694  
 DB 217 AGTGATCTACTGAAAGTGTCTCAGATGACTAATATTATGCTATAGTTAA 171

RESULT 6

US-10-033-528-1176/c  
 Sequence 1176, Application US/10033528  
 Patent No. US20020131971A1  
 GENERAL INFORMATION:  
 APPLICANT: King, Gordon E.  
 APPLICANT: Meagher, Madeleine Joy  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Secrist, Heather  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 FILE REFERENCE: 210121.547C1  
 CURRENT APPLICATION NUMBER: US/10/033.528  
 CURRENT FILING DATE: 2001-12-26  
 NUMBER OF SEQ ID NOS: 1896  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1176  
 LENGTH: 435  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-033-528-1176

Query Match 9.4% Score 167; DB 12; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-76;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 TGTTCCGAGAAATTAATCTTAAATCTGTCTAAATAGAACTTGAACCATTAAGTAA 1587  
 DB 337 TGTTCCGAGAAATTAATCTTAAATCTGTCTAAATAGAACTTGAACCATTAAGTAA 278  
 QY 1588 CAGAACTGCCAATCAGGGCCTAGTTCTTATTAATAATTTGAATAAATAAG 1647  
 DB 277 CAGAACTGCCAATCAGGGCCTAGTTCTTATTAATAATTTGAATAAATAAG 218  
 QY 1648 AGTGATCTACTGAAAGTGTCTCAGATGACTAATATTATGCTATAGTTAA 1694  
 DB 217 AGTGATCTACTGAAAGTGTCTCAGATGACTAATATTATGCTATAGTTAA 171

RESULT 7

US-09-800-729-23  
 Sequence 23, Application US/09800729  
 Patent No. US20020308319A1  
 GENERAL INFORMATION:  
 APPLICANT: Ni et al.  
 TITLE OF INVENTION: 32 Human secreted proteins  
 FILE REFERENCE: P2044P1  
 CURRENT APPLICATION NUMBER: US/09/800.729  
 CURRENT FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: PCT/US00/26013  
 PRIOR FILING DATE: 2000-09-22  
 PRIOR APPLICATION NUMBER: 50/155,709  
 PRIOR FILING DATE: 1999-09-24  
 NUMBER OF SEQ ID NOS: 217  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 23  
 LENGTH: 922  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (6)

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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (885)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (886)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (907)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-23

Query Match
Best Local Similarity 100.0%; Score 80; DB 10; Length 922;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGACATCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 35 AGCTGACATCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 94
|||||

QY 61 AATTCGGCAGCAGCGAGGA 80
|||||
Db 95 AATTCGGCAGCAGCGAGGA 114
|||||

RESULT 8
US-09-764-853-148
; Sequence 148, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 148
; LENGTH: 1772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1772)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-148

Query Match
Best Local Similarity 100.0%; Score 76; DB 10; Length 1772;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTTAACTTCCACCGGCTAGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 42 AGTTTAACTTCCACCGGCTAGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 101
|||||

QY 61 AATTCGGCAGCAGCGG 75
|||||
Db 102 AATTCGGCAGCAGCGG 117
|||||

RESULT 9
US-09-764-870-182
; Sequence 182, Application US/09764870
; Patent No. US20020042396A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 182
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 182
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE

Query Match
Best Local Similarity 100.0%; Score 75; DB 10; Length 1355;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 911 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 852
|||||

QY 61 AATTCGGCAGCAGCG 75
|||||
Db 851 AATTCGGCAGCAGCG 837
|||||

RESULT 10
US-09-764-853-404/c
; Sequence 404, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 404
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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LOCATION: (1346)  
OTHER INFORMATION: n equals a.t.g. or c  
US-09-764-853-404

Query Match 4.2%; Score 75; DB 10; Length 1355;  
Best Local Similarity 100.0%; Pred. No. 8.4e-29;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTACTGGATCGGGGGGGCTGGAAAG 40  
|||||  
DB 911 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTACTGGATCGGGGGGGCTGGAAAG 40  
|||||  
QY 61 AATTCGGCAGGACC 75  
|||||  
DB 851 AATTCGGCAGGACC 837

## RESULT 11

US-09-925-301-686  
Sequence 686, Application US/09925301  
Patent No US20020052308A1

## GENERAL INFORMATION:

APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 686

LENGTH: 496

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (358)

OTHER INFORMATION: n equals a.t.g. or c

NAME/KEY: misc\_feature

LOCATION: (417)

OTHER INFORMATION: n equals a.t.g. or c

NAME/KEY: misc\_feature

LOCATION: (460)

OTHER INFORMATION: n equals a.t.g. or c

NAME/KEY: misc\_feature

LOCATION: (472)

OTHER INFORMATION: n equals a.t.g. or c

NAME/KEY: misc\_feature

LOCATION: (481)

OTHER INFORMATION: n equals a.t.g. or c

NAME/KEY: misc\_feature

LOCATION: (488)

OTHER INFORMATION: n equals a.t.g. or c

US-09-925-301-686

Query Match 4.2%; Score 74; DB 10; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.6e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTACTGGATCGGGGGGGCTGGAAAG 40  
|||||  
DB 18 AGCTGGAGCTCCACCGGGTGGGGGGGGCTCTAGAACTACTGGATCGGGGGGGCTGGAAAG 40  
|||||  
QY 61 AATTCGGCAGGACC 74  
|||||  
DB 78 AATTCGGCAGGACC 91

## RESULT 12

US-09-908-711-28

Sequence 28, Application US/09908711  
Patent No US20020045230A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PA128  
CURRENT APPLICATION NUMBER: US/09/908,711  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US01/01360  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,867  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01344  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,892  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01345  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,888  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01329  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,905  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01354  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,891  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01339  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,869  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01340  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,874  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01334  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,898  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01320  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,853  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01349  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,902  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01239  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,870  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01348  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,882  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01347  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,896  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01307  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,864  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01341  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,856  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01336  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 09/764,868  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US01/01312

;; PRIOR FILING DATE: 2001-01-17  
;; PRIOR APPLICATION NUMBER: 60/179,065  
;; PRIOR FILING DATE: 2000-01-31  
;; PRIOR APPLICATION NUMBER: 60/180,628  
;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: 60/209,467  
;; PRIOR FILING DATE: 2000-06-07  
;; NUMBER OF SEQ ID NOS: 167  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 28  
;; LENGTH: 640  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (555)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (634)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (638)  
;; OTHER INFORMATION: n equals a,t,g, or c  
US-09-908-711-28

Query Match 4.2%; Score 74; DB 10; Length 640;  
Best Local Similarity 100.0%; Pred. No. 2.6e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
|||||  
Db 38 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 97  
|||||  
QY 61 AATTCGGCAGCAGC 74  
|||||  
Db 98 AATTCGGCAGCAGC 111  
|||||

RESULT 13  
US-09-764-853-172  
;; Sequence 172, Application US/09764853  
;; Patent No. US20020090672A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PJ206  
;; CURRENT APPLICATION NUMBER: US/09/764,853  
;; PRIOR FILING DATE: 2001-01-17  
;; Prior application data removed - consult PALM or file wrapper  
;; NUMBER OF SEQ ID NOS: 939  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 172  
;; LENGTH: 737  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (1)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (4)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (5)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (6)  
;; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-853-172

Query Match 4.2%; Score 74; DB 10; Length 737;  
Best Local Similarity 100.0%; Pred. No. 2.7e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
|||||  
Db 48 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 107  
|||||  
QY 61 AATTCGGCAGCAGC 74  
|||||  
Db 108 AATTCGGCAGCAGC 121  
|||||

RESULT 14  
US-09-764-853-305  
;; Sequence 305, Application US/09764853  
;; Patent No. US20020090672A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PJ206  
;; CURRENT APPLICATION NUMBER: US/09/764,853  
;; PRIOR FILING DATE: 2001-01-17  
;; Prior application data removed - consult PALM or file wrapper  
;; NUMBER OF SEQ ID NOS: 939  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 305  
;; LENGTH: 791  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (694)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (764)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (778)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (788)  
;; OTHER INFORMATION: n equals a,t,g, or c  
;; NAME/KEY: SITE  
;; LOCATION: (789)  
;; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-853-305

Query Match 4.2%; Score 74; DB 10; Length 791;  
Best Local Similarity 100.0%; Pred. No. 2.7e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
|||||  
Db 40 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 99  
|||||  
QY 61 AATTCGGCAGCAGC 74  
|||||  
Db 100 AATTCGGCAGCAGC 113  
|||||

RESULT 15  
US-09-764-853-365  
;; Sequence 365, Application US/09764853  
;; Patent No. US20020090672A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PJ206  
;; CURRENT APPLICATION NUMBER: US/09/764,853  
;; PRIOR FILING DATE: 2001-01-17  
;; Prior application data removed - consult PALM or file wrapper  
;; NUMBER OF SEQ ID NOS: 939  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 365  
;; LENGTH: 796

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (763)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (768)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (787)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-365

Query Match          4.2% Score 74; DB 10; Length 756;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTAGTATCGGCTGGCAGG 60
Db 32 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTAGTATCGGCTGGCAGG 61
QY 61 AATTCGGCAGCAGC 74
Db 92 AATTCGGCAGCAGC 105

RESULT 16
US-09-764-898-50
; Sequence 50, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (816)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-898-50

Query Match          4.2% Score 74; DB 10; Length 852;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTAGTATCGGCTGGCAGG 60
Db 43 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTAGTATCGGCTGGCAGG 104
QY 61 AATTCGGCAGCAGC 74
Db 103 AATTCGGCAGCAGC 116

RESULT 17
US-09-764-898-123/c
; Sequence 123, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

```
; FILE REFERENCE: PJ201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (851)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-898-123

Query Match          4.2% Score 74; DB 10; Length 852;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTAGTATCGGCTGGCAGG 60
Db 810 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTAGTATCGGCTGGCAGG 751
QY 61 AATTCGGCAGCAGC 74
Db 750 AATTCGGCAGCAGC 737

RESULT 18
US-09-410-194-14
; Sequence 14, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (394)...(1056)
US-09-410-194-14

Query Match          4.2% Score 74; DB 10; Length 1190;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGCTGCGGCTCTAGAACTAGTAGTATCGGCTGGCAGG 60
```

DL 35 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 94  
|||||  
QY 61 AATTCGGCAGCAGC 74  
|||||  
Db 95 AATTCGGCAGCAGC 108  
|||||

RESULT 19  
US-09-764-864-91  
; Sequence 91, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764.864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 91  
; LENGTH: 1454  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-864-91

Query Match 4.2%, Score 74; DB 10; Length 1454;  
Best Local Similarity 100.0%; Pred. No. 2.8e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60  
|||||  
Db 10 AGCTGAGCTTCACCGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60  
|||||  
QY 61 AATTCGGCAGCAGC 74  
|||||  
Db 70 AATTCGGCAGCAGC 83  
|||||

RESULT 20  
US-09-764-870-217  
; Sequence 217, Application US/09764870  
; Patent No. US20020042386A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT214  
; CURRENT APPLICATION NUMBER: US/09/764.870  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 646  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 217  
; LENGTH: 1707  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1419)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-870-217

Query Match 4.2%, Score 74; DB 10; Length 1707;  
Best Local Similarity 100.0%; Pred. No. 2.8e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60  
|||||  
Db 39 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 98  
|||||

QY 61 AATTCGGCAGCAGC 74  
|||||  
Db 99 AATTCGGCAGCAGC 112  
|||||

RESULT 21  
US-09-764-898-40  
; Sequence 40, Application US/09764898  
; Patent No. US20020090673A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ201  
; CURRENT APPLICATION NUMBER: US/09/764.898  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 1788  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-898-40

Query Match 4.2%, Score 74; DB 10; Length 1788;  
Best Local Similarity 100.0%; Pred. No. 2.8e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 60  
|||||  
Db 31 AGCTGAGCTTCACCGCGGCGGCTCTAGAACTAGTGGATCCCGGCTGACG 90  
|||||  
QY 61 AATTCGGCAGCAGC 74  
|||||  
Db 91 AATTCGGCAGCAGC 104  
|||||

RESULT 22  
US-09-764-903-22  
; Sequence 22, Application US/09764903  
; Patent No. US20020090674A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT228  
; CURRENT APPLICATION NUMBER: US/09/764.903  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 2005  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (4)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (84)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (85)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (259)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1898)

; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1445)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1967)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-903-22

Query Match 4.2%; Score 74; DB 10; Length 2458;  
Best Local Similarity 100.0%; Pred. No. 2 8e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60  
|||||  
Db 330 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 389

QY 61 AATTCGGCAGGAC 74  
|||||  
Db 390 AATTCGGCAGGAC 403

## RESULT 23

US-09-764-864-78  
; Sequence 78, Application US/09764864  
; Patent No. US20020132753A1

## GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PT223

; CURRENT APPLICATION NUMBER: US/09/764,864

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1792

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 78

; LENGTH: 2458

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (4)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (6)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (7)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (11)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-864-78

Query Match 4.2%; Score 74; DB 10; Length 2458;  
Best Local Similarity 100.0%; Pred. No. 2 8e-28;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60  
|||||  
Db 50 AGCTGAGCTCTACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 109

QY 61 AATTCGGCAGGAC 74  
|||||  
Db 110 AATTCGGCAGGAC 123

## RESULT 24

US-09-764-860-248/c  
; Sequence 248, Application US/09764860  
; Patent No. US20020094953A1

## GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008  
; CURRENT APPLICATION NUMBER: US/09/764,860  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 248  
; LENGTH: 367  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: SITE

; LOCATION: (345)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-860-248

Query Match 4.1%; Score 73; DB 10; Length 367;  
Best Local Similarity 100.0%; Pred. No. 8 4e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60  
|||||  
Db 334 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 275

QY 61 AATTCGGCAGGAC 73  
|||||  
Db 274 AATTCGGCAGGAC 262

## RESULT 25

US-09-764-855-67

; Sequence 67, Application US/09764855

; Patent No. US20020119919A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: P110

; CURRENT APPLICATION NUMBER: US/09/764,855

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 67

; LENGTH: 421

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (6)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE

; LOCATION: (12)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-855-67

Query Match 4.1%; Score 73; DB 10; Length 421;  
Best Local Similarity 100.0%; Pred. No. 8 5e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 60  
|||||  
Db 28 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGCTGCAGG 87

QY 61 AATTCGGCAGGAC 73  
|||||  
Db 88 AATTCGGCAGGAC 100

## RESULT 26

```
US-09-925-301-619
; Sequence 619, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 619
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (371)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (440)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (492)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (500)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (537)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (554)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (584)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (587)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-619

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 604;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGTGCAGG 60
Db 28 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGTGCAGG 87

Qy 61 AATTCGGCAGCAG 73
Db 88 AATTCGGCAGCAG 100

RESULT 27
US-09-764-853-136
; Sequence 136, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
```

```
US-09-925-301-619
; Sequence 619, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (525)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (539)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (553)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-136

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 618;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGTGCAGG 60
Db 3 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGTGCAGG 62

Qy 61 AATTCGGCAGCAG 73
Db 63 AATTCGGCAGCAG 75

RESULT 28
US-09-764-853-377
; Sequence 377, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 377
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (614)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (615)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (616)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-377

Query Match
Best Local Similarity 100.0%; Score 73; DB 10; Length 618;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGTGCAGG 60
Db 38 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGGTGCAGG 97

Qy 61 AATTCGGCAGCAG 73
Db 61 AATTCGGCAGCAG 73
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Db 98 AATCGGCACGAG 110
RESULT 29
US-09-764-898-126
: Sequence 126, Application US/09764898
: Patent No. US20020090673A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P201
: CURRENT APPLICATION NUMBER: US-09-764 898
: PRIOR FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 311
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 126
: LENGTH: 618
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (614)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (615)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (616)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-898-126
Query Match 4.1%; Score 73; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 38 AGCTGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 97
QY 61 AATCGGCACGAG 73
|||||
Db 98 AATCGGCACGAG 110
RESULT 30
US-09-908-711-29
: Sequence 29, Application US/09908711
: Patent No. US20020045230A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P129
: CURRENT APPLICATION NUMBER: US/09-908,711
: CURRENT FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: US01/01360
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: 09/764,867
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: US01/01344
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: 09/764,892
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: US01/01345
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: 09/764,888
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: US01/01329
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: 09/764,905
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: US01/01354
: PRIOR FILING DATE: 2001-01-17
Query Match 4.1%; Score 73; DB 10; Length 631;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 20 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 79
US-09-908-711-29
: OTHER INFORMATION: n equals a,t,g, or c
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 29
: LENGTH: 631
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (624)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-908-711-29
Query Match 4.1%; Score 73; DB 10; Length 631;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 73, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
|||||
Db 20 AGCTGGAGCTCCACCGCGGTGGCGGCTCTAGAACTAGTGGATCCCGGGCTGCAGG 79
```

```
QY 61 AATTCGGCACGAG 73
      |||||||
Db 80 AATTCGGCACGAG 92

RESULT 31
US-09-764-898-84
: Sequence 84, Application US/09764898
: Patent No. US2002009073A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P201
: CURRENT APPLICATION NUMBER: US/09/764,898
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 311
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 84
: LENGTH: 647
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (16)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (26)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (32)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (36)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (644)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (645)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (646)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (647)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-898-84

Query Match
Best Local Similarity 4.1%; Score 73; DB 10; Length 647;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGGTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||||
Db 42 AGCTGGAGCTCCACCGCGGTGGGTCTAGAACTAGTGGATCCCGGGCTGCAGG 101

QY 61 AATTCGGCACGAG 73
      |||||||
Db 102 AATTCGGCACGAG 114

RESULT 32
US-09-764-887-129
: Sequence 129, Application US/09764887
: Patent No. US20020042096A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PALL3
: CURRENT APPLICATION NUMBER: US/09/764,887
: CURRENT FILING DATE: 2001-01-17
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: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 658
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 129
: LENGTH: 771
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (558)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (607)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (722)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (758)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-887-129

Query Match
Best Local Similarity 4.1%; Score 73; DB 10; Length 771;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGGTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||||
Db 16 AGCTGGAGCTCCACCGCGGTGGGTCTAGAACTAGTGGATCCCGGGCTGCAGG 75

QY 61 AATTCGGCACGAG 73
      |||||||
Db 76 AATTCGGCACGAG 88

RESULT 33
US-09-764-864-289
: Sequence 289, Application US/09764864
: Patent No. US20020132759A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT223
: CURRENT APPLICATION NUMBER: US/09/764,864
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 1792
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 289
: LENGTH: 869
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (806)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (833)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (865)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-289

Query Match
Best Local Similarity 4.1%; Score 73; DB 10; Length 869;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGGTCTAGAACTAGTGGATCCCGGGCTGCAGG 60
      |||||||
Db 3 AGCTGGAGCTCCACCGCGGTGGGTCTAGAACTAGTGGATCCCGGGCTGCAGG 62

QY 61 AATTCGGCACGAG 73
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Db 63 AATTGGCAGG 75
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RESULT 34
US-09-789-561-58
; Sequence 58, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-789-561-58

Query Match 4.1%; Score 73; DB 10; Length 975;
Best Local Similarity 100.0%; Pred. No. 8.9e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
Db 20 ACCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
|||||
QY 61 AATTGGCAGG 73
|||||
Db 80 AATTGGCAGG 92
|||||

RESULT 35
US-09-764-898-54
; Sequence 54, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 1066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-764-898-54

Query Match 4.1%; Score 73; DB 10; Length 1066;
Best Local Similarity 100.0%; Pred. No. 8.9e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
Db 1 ACCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
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QY 61 AATTGGCAGG 73
|||||
Db 54 AATTGGCAGG 106
|||||

RESULT 36
US-09-925-300-639
; Sequence 639, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 639
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: misc feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: misc feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: misc feature
; LOCATION: (29)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-925-300-639

Query Match 4.1%; Score 73; DB 10; Length 1427;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
Db 34 AGCTGGAGCTCCACCGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
|||||
QY 61 AATTGGCAGG 73
|||||
Db 54 AATTGGCAGG 106
|||||

RESULT 37
US-09-764-853-308/c
; Sequence 308, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 308
; LENGTH: 1511
; TYPE: DNA
; ORGANISM: Homo sapiens
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;  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 770  
; LENGTH: 1637  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-300-770

Query Match 4.1%; Score 73; DB 10; Length 1637;  
Best Local Similarity 100.0%; Pred. No. 9.1e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTGTATATAATTAGTGGATCCCGCGGCTGCAGG 60  
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DB 4 AGCTGGAGCTCCACCGCGGTGGCGGCTGTATATAATTAGTGGATCCCGCGGCTGCAGG 60  
  
QY 61 AATTCGGCAGGAG 73  
|||||  
DB 64 AATTCGGCAGGAG 76

RESULT 42  
US-09-862-027-13  
; Sequence 13, Application US/09862027  
; Patent No. US20020142428A1  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.  
; TITLE OF INVENTION: No. US20020142428A1 Kinases and Uses Thereof  
; FILE REFERENCE: 35800/234862  
; CURRENT APPLICATION NUMBER: US/09/862,027  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US/09/345,473  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1737  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (275)....(1522)  
US-09-862-027-13

Query Match 4.1%; Score 73; DB 10; Length 1737;  
Best Local Similarity 100.0%; Pred. No. 9.1e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCTGTATATAATTAGTGGATCCCGCGGCTGCAGG 60  
|||||  
DB 2 AGCTGGAGCTCCACCGCGGTGGCGGCTGTATATAATTAGTGGATCCCGCGGCTGCAGG 60  
  
QY 61 AATTCGGCAGGAG 73  
|||||  
DB 81 AATTCGGCAGGAG 93

RESULT 43  
US-09-739-254-32  
; Sequence 32, Application US/09739254  
; Patent No. US20010021700A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 49 Human Secreted Proteins  
; FILE REFERENCE: P2032P1

;  
; CURRENT APPLICATION NUMBER: US/09/739,254  
; CURRENT FILING DATE: 2000-12-19  
; EARLIER APPLICATION NUMBER: 09/511,554  
; EARLIER FILING DATE: 2000-02-23  
; EARLIER APPLICATION NUMBER: PCT/US99/19330  
; EARLIER FILING DATE: 1999-08-24  
; EARLIER APPLICATION NUMBER: 60/097,917  
; EARLIER FILING DATE: 1998-08-25  
; EARLIER APPLICATION NUMBER: 60/098,634  
; EARLIER FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 1906  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (617)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (940)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1461)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1901)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-739-254-32

Query Match 4.1%; Score 73; DB 10; Length 1906;  
Best Local Similarity 100.0%; Pred. No. 9.2e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 CTGGAGCTCCACCGCGGTGGCGGCTGTATATAATTAGTGGATCCCGCGGCTGCAGGAA 62  
|||||  
DB 2 CTGGAGCTCCACCGCGGTGGCGGCTGTATATAATTAGTGGATCCCGCGGCTGCAGGAA 61  
  
QY 63 TTGGGCAGGAGCC 75  
|||||  
DB 62 TTGGGCAGGAGCC 74

RESULT 44  
US-09-904-615-32  
; Sequence 32, Application US/09904615  
; Patent No. US20020026040A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 49 Human Secreted Proteins  
; FILE REFERENCE: P2032P1  
; CURRENT APPLICATION NUMBER: US/09/904,615  
; PRIOR FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 09/511,554  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/097,917  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: 60/098,634  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 1906  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (617)  
; OTHER INFORMATION: n equals a,t,g, or c



US-09-764-853-380  
; Sequence 380, Application US/09764853  
; Patent No. US20020090672A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P206  
; CURRENT APPLICATION NUMBER: US/09/764,853  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 939  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 380  
; LENGTH: 2596  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: n equals a.t.g, or c  
; NAME/KEY: SITE  
; LOCATION: (2508)  
; OTHER INFORMATION: n equals a.t.g, or c  
; NAME/KEY: SITE  
; LOCATION: (2529)  
; OTHER INFORMATION: n equals a.t.g, or c  
; NAME/KEY: SITE  
; LOCATION: (2556)  
; OTHER INFORMATION: n equals a.t.g, or c  
US-09-764-853-380

Query Match 4.1%, Score 73; DB 10; Length 2596;  
Best Local Similarity 100.0%; Pred. No. 9.3e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
Db 33 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
QY 61 AATTCGGCAGCAG 73  
Db 93 AATTCGGCAGCAG 105

RESULT 49  
US-09-764-898-128  
; Sequence 128, Application US/09764898  
; Patent No. US20020090673A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P201  
; CURRENT APPLICATION NUMBER: US/09/764,898  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 128  
; LENGTH: 2596  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: n equals a.t.g, or c  
; NAME/KEY: SITE  
; LOCATION: (2508)  
; OTHER INFORMATION: n equals a.t.g, or c  
; NAME/KEY: SITE  
; LOCATION: (2529)  
; OTHER INFORMATION: n equals a.t.g, or c  
; NAME/KEY: SITE  
; LOCATION: (2556)

; OTHER INFORMATION: n equals a.t.g, or c  
US-09-764-898-128

Query Match 4.1%, Score 73; DB 10; Length 2596;  
Best Local Similarity 100.0%; Pred. No. 9.3e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
Db 33 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 92  
QY 61 AATTCGGCAGCAG 73  
Db 93 AATTCGGCAGCAG 105

RESULT 50  
US-09-789-561-64  
; Sequence 64, Application US/09789561  
; Patent No. US20020064818A1  
; GENERAL INFORMATION:  
; APPLICANT: NI et al.  
; TITLE OF INVENTION: 52 Human secreted proteins  
; FILE REFERENCE: P2043P1  
; CURRENT APPLICATION NUMBER: US/09/789,561  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/24008  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/152,317  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/152,315  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 2751  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-789-561-64

Query Match 4.1%, Score 73; DB 10; Length 2751;  
Best Local Similarity 100.0%; Pred. No. 9.4e-28;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60  
Db 24 AGCTGGAGCTCCACCGCGGTGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 83  
QY 61 AATTCGGCAGCAG 73  
Db 84 AATTCGGCAGCAG 96

Search completed: October 31, 2002, 12:44:30  
Job time : 80 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 10:10:50 : Search time 64 Seconds  
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8500 696 Million cell updates/sec

Title: US-09-854-300-7

Perfect score: 1774

Sequence: 1 agctggagctccaccgcggt..... atagggaagtcttctctctcag 1774

Scoring table: OLIGO\_NTC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

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Post-processing: Listing first 75 summaries

Database : Issued\_Patents\_NA.\*

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- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	77	4.3	912	2	US-09-090-567-3
2	74	4.2	2605	2	US-08-680-395-4
3	73	4.1	545	4	US-09-227-357-125
4	73	4.1	1378	1	US-08-075-533-20
5	73	4.1	1378	2	US-08-948-176-20
6	73	4.1	1378	5	PCT-US91-09160-20
7	73	4.1	1556	4	US-09-043-937A-3
8	73	4.1	1568	4	US-09-043-937A-1
9	73	4.1	1585	4	US-09-183-861-54
10	73	4.1	1585	4	US-09-022-765-54
11	73	4.1	2775	1	US-08-730-771-1
12	73	4.1	2775	4	US-09-060-208-1
13	73	4.1	3089	1	US-08-472-934-5
14	73	4.1	3089	2	US-08-723-460A-5
15	73	4.1	3089	2	US-08-461-146C-5
16	73	4.1	3089	3	US-08-461-145C-5
17	73	4.1	3089	4	US-08-638-823-3
18	73	4.1	3328	4	US-08-960-048-1
19	73	4.0	2045	4	US-08-795-088A-1
20	70	3.9	2085	2	US-08-668-128E-7
21	70	3.9	2085	2	US-08-905-445-7
22	67	3.8	500	4	US-08-818-112-101
23	67	3.8	500	4	US-08-818-111-96
24	67	3.8	500	4	US-09-056-556-101
25	67	3.8	500	4	US-09-072-596-96
26	66	3.7	752	4	US-08-976-259-108
27	66	3.7	849	3	US-08-646-538-14

28	66	3.7	849	4	US-09-503-222-14	Sequence 14, Appl
29	66	3.7	1924	4	US-09-424-283-5	Sequence 5, Appl
30	66	3.7	1958	4	US-09-215-221-9	Sequence 9, Appl
31	66	3.7	2961	4	US-08-446-935-6	Sequence 6, Appl
32	66	3.7	3699	3	US-08-646-538-6	Sequence 6, Appl
33	66	3.7	3699	4	US-09-503-222-6	Sequence 6, Appl
34	66	3.7	3792	2	US-08-992-334-1	Sequence 1, Appl
35	66	3.7	3792	3	US-08-302-752-1	Sequence 2, Appl
36	66	3.7	5234	2	US-08-992-334-2	Sequence 1, Appl
37	66	3.7	5234	3	US-08-302-752-2	Sequence 2, Appl
38	66	3.7	6045	3	US-08-675-566-18	Sequence 18, Appl
39	66	3.7	6244	3	US-08-675-566-17	Sequence 17, Appl
40	66	3.7	6447	3	US-08-675-566-16	Sequence 16, Appl
41	66	3.7	6578	3	US-08-675-566-15	Sequence 15, Appl
42	66	3.7	6612	3	US-08-675-566-14	Sequence 14, Appl
43	66	3.7	6722	3	US-08-302-752-3	Sequence 3, Appl
44	66	3.7	6722	3	US-08-675-566-2	Sequence 2, Appl
45	66	3.7	6958	3	US-08-675-566-1	Sequence 1, Appl
46	66	3.7	6994	3	US-08-675-566-3	Sequence 3, Appl
47	66	3.7	7001	3	US-08-659-206A-1	Sequence 1, Appl
48	66	3.7	7287	2	US-08-818-112-14	Sequence 14, Appl
49	65	3.7	1058	4	US-08-818-111-14	Sequence 14, Appl
50	65	3.7	1058	4	US-09-056-556-14	Sequence 14, Appl
51	65	3.7	1058	4	US-09-072-596-14	Sequence 14, Appl
52	65	3.7	1830	1	US-08-343-733A-2	Sequence 2, Appl
53	65	3.7	2082	4	US-09-233-505-9	Sequence 9, Appl
54	65	3.7	3023	4	US-09-308-022-4	Sequence 4, Appl
55	63	3.6	229	4	US-09-116-492A-39	Sequence 39, Appl
56	63	3.6	278	2	US-08-713-000-10	Sequence 10, Appl
57	63	3.6	278	2	US-08-975-316-10	Sequence 10, Appl
58	63	3.6	278	4	US-09-211-710-10	Sequence 10, Appl
59	63	3.6	278	4	US-09-615-192A-10	Sequence 10, Appl
60	63	3.6	300	1	US-08-644-664B-24	Sequence 24, Appl
61	63	3.6	300	2	US-08-761-277A-24	Sequence 24, Appl
62	63	3.6	803	2	US-08-967-101-117	Sequence 117, App
63	63	3.6	803	2	US-08-592-541-117	Sequence 117, App
64	63	3.6	803	3	US-09-124-698-117	Sequence 117, App
65	63	3.6	803	3	US-09-127-480-117	Sequence 117, App
66	63	3.6	803	4	US-08-496-841C-117	Sequence 117, App
67	63	3.6	803	4	US-09-124-523-117	Sequence 117, App
68	63	3.6	1264	1	US-08-006-082A-1	Sequence 1, Appl
69	63	3.6	2842	1	US-08-175-388-3	Sequence 3, Appl
70	63	3.6	2842	2	US-08-779-620-3	Sequence 3, Appl
71	63	3.6	2842	2	US-08-818-726-3	Sequence 3, Appl
72	63	3.6	3198	4	US-08-842-306B-48	Sequence 48, Appl
73	63	3.6	3198	4	US-08-838-973B-48	Sequence 48, Appl
74	63	3.6	3198	4	US-09-183-861-48	Sequence 48, Appl
75	62	3.5	1053	4		

#### ALIGNMENTS

RESULT 1  
US-09-090-567-3  
; Sequence 3, Application US/09090567  
; Patent No. 5989549  
; GENERAL INFORMATION:  
; APPLICANT: Sullivan, Robert  
; APPLICANT: Prub, Bruno  
; APPLICANT: Lgar, Christine  
; APPLICANT: Gaudreault, Christian  
; TITLE OF INVENTION: Acrosomal Sperm Protein And  
; TITLE OF INVENTION: Uses Thereof  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swabey Ogilvy Renault  
; STREET: 1600 - 1381 McGill College  
; CITY: Montreal  
; STATE: QC  
; COUNTRY: Canada  
; ZIP: H3A 2Y3  
; COMPUTER READABLE FORM:



MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/090,567  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Kevin P  
REGISTRATION NUMBER: 26,674  
REFERENCE/DOCKET NUMBER: 13045-2"US" FC/CC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 514-845-7126  
TELEFAX: 514-288-8389  
TELEX:  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS  
LENGTH: 912 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
US-09-090-567-3

Query Match 4.3%; Score 77; DB 2; Length 912;  
Best Local Similarity 100.0%; Pred. No. 5e-29;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGACTCTACCGGCGGCTGAGTAATATATGATCCCGCGGCTGACG 60  
DB 7 AGCTGAGACTCTACCGGCGGCTGAGTAATATATGATCCCGCGGCTGACG 60  
QY 61 AATCGGACGAGCGCA 77  
DB 67 AATCGGACGAGCGCA 83

RESULT 2  
US-08-680-395-4  
Sequence 4, Application US/08680395  
Patent No. 5892010  
GENERAL INFORMATION:  
APPLICANT: Gray, Joe W  
APPLICANT: Collins, Colin  
APPLICANT: Hwang, Soc-in  
APPLICANT: Godfrey, Tony  
APPLICANT: Kowbel, David  
APPLICANT: Rommens, Johanna  
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/680,395  
FILING DATE: 15-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 024070-06890005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2605 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1, 2605  
OTHER INFORMATION: (note="cDNA clone ccd3 of 4 kb  
OTHER INFORMATION: transcript")  
US-08-680-395-4

Query Match 4.3%; Score 74; DB 2; Length 2605;  
Best Local Similarity 100.0%; Pred. No. 1.6e-27;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGACTCTACCGGCGGCTGAGTAATATATGATCCCGCGGCTGACG 60  
DB 36 AGCTGAGACTCTACCGGCGGCTGAGTAATATATGATCCCGCGGCTGACG 95  
QY 61 AATCGGACGAGC 74  
DB 96 AATCGGACGAGC 109

RESULT 3  
US-09-227-357-125  
Sequence 125, Application US/99227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
EARLIER FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08

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; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,564
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SEQ ID NO 125
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (41)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (87)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-125

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Query Match      4.1%; Score 73; DB 4; Length 545;
Best Local Similarity 100.0%; Pred. NO. 5.1e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
    |||||||
Db 117 AGCTGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 176
    |||||||
QY 61 AATTCGGCAGG 73

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Db 177 AATTCGGCAGG 189
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## RESULT 4

```

US-08-075-533-20
; Sequence 20, Application US/08075533
; Patent No. 5530186
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; TITLE OF INVENTION: Nucleotide Sequences of Soybean Acyl-ACP
; TITLE OF INVENTION: Thioesterase Genes
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,533
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/531,264
; FILING DATE: 20-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrissey, Bruce W.
; REGISTRATION NUMBER: 30,663
; REFERENCE/DOCKET NUMBER: CP-8926-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4927
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Brassica napus
US-08-075-533-20

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Query Match      4.1%; Score 73; DB 1; Length 1378;
Best Local Similarity 100.0%; Pred. NO. 5.1e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AATTCGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 60
    |||||||
Db 52 AGCTGAGCTCCACGGGTGGCGGCTCTAGAACTAGTGGATCCCGGCTGCAGG 111
    |||||||
QY 61 AATTCGGCAGG 73
    |||||||
Db 112 AATTCGGCAGG 124

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## RESULT 5

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US-08-948-176-20
; Sequence 20, Application US/08948176
; Patent No. 5945585
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; TITLE OF INVENTION: ACYL-ACP THIOESTERASES GENES

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```

Query Match Similarity      4.1%; Score 73; DB 2; Length 1378;
Best Local Similarity     100.0%; Pred. No. 5, le-27;
Matches    73; Conservative   0; Mismatches    0; Indels    0; Gaps    0;

QY       1 AGCTGAGACCCACCACCGGGGTGGTGGTCCTTAGAAATTATGTGAATCCTTTCTTGTAATGATTAATAAAGT
          |||||||
DB        52 AGCTGAGAGCTCAACCGGGGTGGTGGGCCTCTTAGAACACTAGTGGATGCCCTCGGCGTGGAGG 111
          |||||||

QY       61 ATTCTGGCACGAG 73
          |||||||
DB       112 AATTCGSCACGAG 124

RESULT 6
PCT-US91 -09160-20
Sequence 20 Application FC/TUSyUJ09150
GENERAL INFORMATION.
APPLICANT: Hitz, William D.
APPLICANT: Yadav, Narendra S.
TITLE OF INVENTION: Nucleotide Sequences of Soybean Acyl-ACP
TITLE OF INVENTION: Thioesterase Genes
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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```

Query Match 4.1% Score 73 DB 5 Length 1378:
Best Local Similarity 100.0% Pred. 5.1e-27:
Matches 73 Conservative 0 Mismatches 0 Indels 0 Gaps 0

C: 1 ACGTGGAGCTCCACCGCGGCTGCTTATGAAATAGTGATCCGCTGCTGAG 66
Db 52 ACGTGGAGCTCCACCGCGGCTGCTTATGAAATAGTGATCCGCTGCTGAG 111
    |||
OY 61 AATTCGACACGAG 73
    |||
Db 112 AATTCGACACGAG 124

```

RESULT 7  
 US-09-043-937A-3  
 Sequence 3, Application US/09043937A  
 Patent No. 6211432  
 GENERAL INFORMATION:  
 APPLICANT: BOUDET, ALAIN-MICHEL  
 PICHON, MAGALIE  
 GRIMA-PETENATI, JACQUELINE  
 BECKERT, MICHEL  
 GAMAS, PASCAL  
 BRAT, JEAN-FRANCOIS  
 TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-CoA  
 REDUCTASE, AND APPLICATIONS THEREOF IN THE CONTROL OF  
 LIGNIN CONTENTS IN PLANTS  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHAYE, P. C.  
 STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/043,937A  
 FILING DATE: 24-Jul-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR96/01544





```

1  NUMBER OF SEQUENCES: 1
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Ratner & Prestia
4  STREET: P.O. Box 980
5  CITY: Valley Forge
6  STATE: PA
7  COUNTRY: USA
8  ZIP: 19482-0980
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Diskette
11 COMPUTER: IBM Compatible
12 OPERATING SYSTEM: DOS
13 SOFTWARE: FastSeq Version 1.5
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US-09-060-208-1
16 FILING DATE: April 15, 1998
17 CLASSIFICATION:
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER:
20 FILING DATE:
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Prestia, Paul F.
23 REGISTRATION NUMBER: 23,031
24 REFERENCE/DOCKET NUMBER: P50380-1
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 610-407-0700
27 TELEFAX: 610-407-0701
28 TELEX: 846169
29 INFORMATION F# SEQ ID NO: 1:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 2775 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: CDNA
36 HYPOTHETICAL: NO
37 ANTI-SENSE: NO
38 FRAGMENT TYPE:
39 ORIGINAL SOURCE:
40 US-09-060-208-1

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Query Match	4.1%	Score 73	DB 4	Length 2775
Best Local Similarity	100.0%	Pred. No. 5	le-27	
Matches 73	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	AGCTGGAGCTCCACGGCGGTGGGGGGGTCTTAAACTATGTCGATCGCCCGCTTCTGAGG	50		
Db	AGCTGGAGCTCCACGGCGGTGGGGGGGTCTTAAACTATGTCGATCGCCCGCTTCTGAGG	50		
QY 61	AATTCGGCAGGAG	73		
Db	AATTCGGCAGGAG	109		

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: RESULT 13
: US-08-472-934-5
: Sequence 5, Application US/08472934
: Patent No. 5753446
: GENERAL INFORMATION:
: APPLICANT: JOHNSON, GARY L.
: TITLE OF INVENTION: METHOD AND H
: TITLE OF INVENTION: RESPONSIVEN
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lahive and Cocklie
: STREET: 60 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02109
: COMPUTER FILEABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible

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1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: PatentIn Release #1.0, Version #1.25
3
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/08/472,934
6 FILING DATE: 08-JUN-1995
7 CLASSIFICATION: 435
8
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 08/440,421
11 FILING DATE: 15-MAY-1995
12
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: 08/354,516
15 FILING DATE: 21-FEB-1995
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 5,405,941
19 FILING DATE: 15-APR-1993
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/323,460
23 FILING DATE: 14-OCT-1994
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: PCT/US94/11690
27 FILING DATE: 14-OCT-1994
28
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: PCT/US94/04178
31 FILING DATE: 15-APR-1994
32
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Giulio A. DeConti, Jr. Esq.
35 REGISTRATION NUMBER: 31,503
36 REFERENCE/DOCKET NUMBER: CFI-004DVCP2
37
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: (617) 227-7400
40 TELEFAX: (617) 227-5941
41
42 INFORMATION FOR SEQ ID NO: 5:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 3089 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: double
47 TOPOLOGY: linear
48 MOLECULE TYPE: cDNA
49 FEATURE:
50 NAME/KEY: CDS
51 LOCATION: 400...2280
52
53 US-08-472-934-5

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Query Match      4.1%; Score 73; DB 1; Length 3089;
Best local Similarity 100.0%; Pred. No. 5.le-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTGAGACTCACCGCGGCGGGCGGCGGCTCTATAAATTATGATCCCGCGGCTGCAGG 60
Db 11 AACTGAGACTCACCGAGGCTGGGCGGCGGCTCTATAAATTATGATCCCGCGGCTGCAGG 70

QY 61 AATTGGCCACGAG 73
Db 71 AATTGGCCACGAG 83

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RESULT 14  
US-08-323-460A-5  
; Sequence 5, Application US/08323460A  
; Patent No. 5854043  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, GARY L.  
; TITLE OF INVENTION: METHOD AND PRODUCT FOR PERCUSSING CELL  
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
; STREET: 1700 LINCOLN STREET, SUITE 3500  
; CITY: DENVER  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80203  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,460A  
FILING DATE: 14-OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILING DATE: 14-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOVARIK, JOSEPH E.  
REGISTRATION NUMBER: 33,005  
REFERENCE/DOCKET NUMBER: 2879-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3089 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 400..2280  
US-08-323-460A-5

Query Match 4.1%; Score 73; DB 2; Length 3089;  
Best Local Similarity 100.0%; Pred. No. 5.1e-27;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGAGCTCCACCGCGGCTGCGGCGCTTACAGACTAGTGGATCCCGGCGTGGAGG 60  
DB 11 ACCTGAGCTCCACCGCGGCTGCGGCGCTTACAGACTAGTGGATCCCGGCGTGGAGG 70  
QY 61 AATCGGCACGAG 73  
DB 71 AATCGGCACGAG 83

RESULT 15  
US-08-461-146C-5  
Sequence 5, Application US/08461146C  
Patent No. 5981265  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahnive and Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,146C  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/354,516  
FILING DATE: 21-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/049,254  
FILING DATE: 15-APR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/323,460  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11690  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04178  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: CPI-004CNS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3089 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 400..2280  
US-08-461-146C-5

Query Match 4.1%; Score 73; DB 2; Length 3089;  
Best Local Similarity 100.0%; Pred. No. 5.1e-27;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGAGCTCCACCGCGGCTGCGGCGCTTACAGACTAGTGGATCCCGGCGTGGAGG 60  
DB 11 ACCTGAGCTCCACCGCGGCTGCGGCGCTTACAGACTAGTGGATCCCGGCGTGGAGG 70  
QY 61 AATCGGCACGAG 73  
DB 71 AATCGGCACGAG 83

RESULT 16  
US-08-461-145C-5  
Sequence 5, Application US/08461145C  
Patent No. 6074861  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, GARY L.  
TITLE OF INVENTION: NOVEL MEKK PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahnive and Cockfield, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:-  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,145C  
FILING DATE: 5-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,254  
FILING DATE: 11-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/323,460  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11690

;; FILING DATE: 14-OCT-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/04178  
;; FILING DATE: 15-APR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/354,516  
;; FILING DATE: 21-FEB-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kara, Catherine J.  
;; REGISTRATION NUMBER: P-41,106  
;; REFERENCE/DOCKET NUMBER: CPI-004CN1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 227-7400  
;; TELEFAX: (617) 227-5941  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3089 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 400..2280  
US-08-461-145C-5

Query Match 4.1%; Score 73; DB 3; Length 3089;  
Best Local Similarity 100.0%; Pred. No. 5.1e-27;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCCGGGCTCAGG 60  
DB 11 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCCGGGCTCAGG 70  
QY 61 AATTCGGCAGG 73  
DB 71 AATTCGGCAGG 83

RESULT 17  
US-08-628-829-5  
;; Sequence 9, Application US/08628829A  
;; Patent No. 633170  
;; GENERAL INFORMATION:  
;; APPLICANT: Johnson, Gary L.  
;; TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External  
;; FILE REFERENCE: CPI-004DVC3  
;; CURRENT APPLICATION NUMBER: US/08/628,829A  
;; CURRENT FILING DATE: 1996-04-05  
;; EARLIER APPLICATION NUMBER: 08/440,421  
;; EARLIER FILING DATE: 1995-05-15  
;; EARLIER APPLICATION NUMBER: 08/323,460  
;; EARLIER FILING DATE: 1994-10-14  
;; EARLIER APPLICATION NUMBER: 08/049,254  
;; EARLIER FILING DATE: 1993-05-15  
;; EARLIER APPLICATION NUMBER: 08/410,402  
;; EARLIER FILING DATE: 1995-04-24  
;; EARLIER APPLICATION NUMBER: 08/472,934  
;; EARLIER FILING DATE: 1995-06-06  
;; NUMBER OF SEQ ID NOS: 25  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 9  
;; LENGTH: 3089  
;; TYPE: DNA  
;; ORGANISM: Mus musculus  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (400)..(2277)  
US-08-628-829-9

Query Match 4.1%; Score 73; DB 4; Length 3089;  
Best Local Similarity 100.0%; Pred. No. 5.1e-27;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCCGGGCTCAGG 60  
DB 11 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCCGGGCTCAGG 70  
QY 61 AATTCGGCAGG 73  
DB 71 AATTCGGCAGG 83

RESULT 18  
US-08-960-048-1  
;; Sequence 1, Application US/08960048C  
;; Patent No. 6271443  
;; GENERAL INFORMATION:  
;; APPLICANT: Stalker, D. et al.  
;; TITLE OF INVENTION: Plant Cellulose Synthase and Promoter  
;; FILE REFERENCE: 15621/01/US  
;; CURRENT APPLICATION NUMBER: US/08/960,048C  
;; CURRENT FILING DATE: 1997-10-29  
;; PRIOR APPLICATION NUMBER: 60/029,987  
;; PRIOR FILING DATE: 1996-10-29  
;; NUMBER OF SEQ ID NOS: 12  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 3328  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic oligonucleotide  
US-08-960-048-1

Query Match 4.1%; Score 73; DB 4; Length 3328;  
Best Local Similarity 100.0%; Pred. No. 5.1e-27;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCCGGGCTCAGG 60  
DB 10 AGCTGGAGCTCCACCGCGGTGGCGCGCTCTAGAACTAGTGGATCCCCGGGCTCAGG 99  
QY 61 AATTCGGCAGG 73  
DB 90 AATTCGGCAGG 102

RESULT 19  
US-08-795-088A-1  
;; Sequence 1, Application US/08795088A  
;; Patent No. 6242569  
;; GENERAL INFORMATION:  
;; APPLICANT: Sul, Hong-Bing  
;; APPLICANT: Goeddel, David V.  
;; TITLE OF INVENTION: Regulators of Apoptosis  
;; NUMBER OF SEQUENCES: 3  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Science & Technology Law Group  
;; STREET: 75 Denise Drive  
;; CITY: Hillsborough  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94010  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-POS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/795,088A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Osman, Richard A



REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: 197-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2045 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-795-088A-1

Query Match 4.0%; Score 71; DB 4; Length 2045;  
Best Local Similarity 100.0%; Pred. No. 5,1e-26;  
Matches 71: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTGGAGCTCACCAGGCGGGGCGGCTCTAGACTAGTGAATCCCGGGCTGCAGAA 62  
DB 10 CTGGAGCTCACCAGGCGGGGCGGCTCTAGAACTAGTGAATCCCGGGCTGCAGAA 69  
QY 63 TTGCGCAGCAG 73  
DB 70 TTGCGCAGCAG 80

RESULT 20  
US-08-668-128B-7  
Sequence 7, Application US/08668.128B  
Patent No. 5840568  
GENERAL INFORMATION:  
APPLICANT: Firenedschub, Michael  
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/668.128B  
FILING DATE: 21-JUNE-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/644,116  
FILING DATE: 10-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/580,980  
FILING DATE: 03-JANUARY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,328  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5840568man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-668-128B-7  
Query Match 3.9%; Score 70; DB 2; Length 2085;  
Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
Matches 70: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAGCTCCACCGGGGCTGAGTGAATGATGATGATGATGATGATGATGATGAT 64  
DB 1 GGAAGCTCCACCGGGGCTGAGTGAATGATGATGATGATGATGATGATGATGAT 60  
QY 65 CGGACAGAGC 74  
DB 61 CGGACAGAGC 70

RESULT 21  
US-08-905-445-7  
Sequence 7, Application US/08905.445  
Patent No. 5864015  
GENERAL INFORMATION:  
APPLICANT: Firenedschub, Michael  
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905.445  
FILING DATE: 04-AUG-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/668,128  
FILING DATE: 21-JUNE-1996  
APPLICATION NUMBER: 08/644,116  
FILING DATE: 10-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/580,980  
FILING DATE: 03-JANUARY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,328  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5864015man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-905-445-7

Query Match 3.9%; Score 70; DB 2; Length 2085;  
Best Local Similarity 100.0%; Pred. No. 1.6e-25;  
Matches 70: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAGCTCCACCGGGGCTGAGTGAATGATGATGATGATGATGATGATGATGAT 64  
DB 1 GGAAGCTCCACCGGGGCTGAGTGAATGATGATGATGATGATGATGATGATGAT 60

QY 65 CGCAGCAGC 74  
 |||||  
 Db 61 CGCAGCAGC 70

## RESULT 22

US-08-818-112-101/c  
 : Sequence 101, Application US/08818112  
 : Patent No. 6290969  
 : GENERAL INFORMATION:  
 : APPLICANT: Reed, Steven G.  
 : APPLICANT: Skeiky, Yasir A.W.  
 : APPLICANT: Dillon, Davin C.  
 : APPLICANT: Campos-Neto, Antonio  
 : APPLICANT: Houghton, Raymond  
 : APPLICANT: Vedvick, Thomas S.  
 : APPLICANT: Twardzik, Daniel R.  
 : TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
 : NUMBER OF SEQUENCES: 153  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: SEED and BERRY LLP  
 : STREET: 6300 Columbia Center, 701 Fifth Avenue  
 : CITY: Seattle  
 : STATE: Washington  
 : COUNTRY: USA  
 : ZIP: 98104-7092  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/818,112  
 : FILING DATE: 13-MAR-1997  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Maki, David J.  
 : REGISTRATION NUMBER: 31,392  
 : REFERENCE/DOCKET NUMBER: 210121.411C6  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (206) 622-4900  
 : TELEFAX: (206) 682-6031  
 : INFORMATION FOR SEQ ID NO: 101:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 500 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : US-08-818-112-101

Query Match 3.8%; Score 67; DB 4; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-24;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCCAGCGGATGCGGCGCTCTAGAACTAGTGGATCCCGGCTGCAGGAATTCG 66  
 |||||  
 Db 500 AGCTCCAGCGGATGCGGCGCTCTAGAACTAGTGGATCCCGGCTGCAGGAATTCG 441  
 QY 67 GCACGAG 73  
 |||||  
 Db 440 GCACGAG 434

## RESULT 23

US-08-818-111-96/c  
 : Sequence 96, Application US/08818111  
 : Patent No. 6338852  
 : GENERAL INFORMATION:  
 : APPLICANT: Reed, Steven G.  
 : APPLICANT: Skeiky, Yasir A.W.  
 : APPLICANT: Dillon, Davin C.  
 : APPLICANT: Campos-Neto, Antonio

APPLICANT: Houghton, Raymond  
 APPLICANT: Vedvick, Thomas S.  
 APPLICANT: Twardzik, Daniel R.  
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS  
 NUMBER OF SEQUENCES: 148  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED and BERRY LLP  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/818,111  
 FILING DATE: 13-MAR-1997  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Maki, David J.  
 REGISTRATION NUMBER: 31,392  
 REFERENCE/DOCKET NUMBER: 210121.417C6  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 96:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 500 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-818-111-96

Query Match 3.8%; Score 67; DB 4; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-24;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCCAGCGGATGCGGCGCTCTAGAACTAGTGGATCCCGGCTGCAGGAATTCG 66  
 |||||  
 Db 500 AGCTCCAGCGGATGCGGCGCTCTAGAACTAGTGGATCCCGGCTGCAGGAATTCG 441  
 QY 67 GCACGAG 73  
 |||||  
 Db 440 GCACGAG 434

## RESULT 24

US-09-056-556-101/c  
 : Sequence 101, Application US/09056556  
 : Patent No. 6350456  
 : GENERAL INFORMATION:

APPLICANT: Reed, Steven G.  
 APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Dillon, Davin C.  
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND  
 NUMBER OF SEQUENCES: 241  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED and BERRY LLP  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/056,556

TRE

FILING DATE: 07-APR-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.457  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-036-556-101

Query Match 3.8%; Score 67; DB 4; Length 500;  
Best Local Similarity 100.0%; Pred. No. 5.3e-24;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 66  
DB 500 AGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 441

QY 67 GCACGAG 73  
DB 440 GCACGAG 434

RESULT 25  
US-09-072-596-96/c  
Sequence 96, Application US/09072596  
Patent No. 6458366  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, David C.  
APPLICANT: Campos-Neto, Antonia  
APPLICANT: Houghton, Raymond  
APPLICANT: Veduglik, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Lodges, Michael J.  
APPLICANT: Hendrickson, Ronald C.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 350  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and HERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,596  
FILING DATE: 05-MAY-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.417C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 500 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-072-596-96

Query Match 3.8%; Score 67; DB 4; Length 500;  
Best Local Similarity 100.0%; Pred. No. 5.3e-24;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 66  
DB 500 AGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGGAATTCG 441

QY 67 GCACGAG 73  
DB 440 GCACGAG 434

RESULT 26  
US-08-976-259-108/c  
Sequence 108, Application US/08976259  
Patent No. 6316609  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Choi, Gil H.  
APPLICANT: Welch, Rodney A.  
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli  
Patent No. 6316609  
NUMBER OF SEQUENCES: 142  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Ave, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,259  
FILING DATE: Herewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953  
ATTORNEY/AGENT INFORMATION:  
NAME: Steife, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2500  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 752 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-976-259-108

Query Match 3.7%; Score 66; DB 4; Length 752;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGG 60  
DB 111 AGCTGAGCTCCACCGCGGTGGCGCGCTAGACTAGTGCATCCCGCGGCTGCAGG 52

QY 61 AATTCG 66  
DB 51 AATTCG 46

```
RESULT 27
US-08-646-538-14
; Sequence 14, Application US/08646538
; Patent No. 6027881
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,538
; FILING DATE: No. 6027881 yet assigned
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..849
; OTHER INFORMATION: /note= "pBSGFPsg11"
US-08-646-538-14

Query Match 3.7%; Score 66; DB 3; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 60
Db 52 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 111
QY 61 AATTCG 66
Db 112 AATTCG 117

RESULT 28
US-09-503-222-14
; Sequence 14, Application US/0950222
; Patent No. 6265548
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
```

```
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,222
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,538
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..849
; OTHER INFORMATION: /note= "pBSGFPsg11"
US-09-503-222-14

Query Match 3.7%; Score 66; DB 4; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 60
Db 52 AGCTGGAGCTCCACCGCGTGGCGCGCTCTAGAACTAGTGGATCCCGCGGTGCAGG 111
QY 61 AATTCG 66
Db 112 AATTCG 117

RESULT 29
US-09-424-283-5/c
; Sequence 5, Application US/09424283
; Patent No. 6437219
; GENERAL INFORMATION:
; APPLICANT: Grimes, et al.
; TITLE OF INVENTION: Sucrose binding proteins
; FILE REFERENCE: 4630-50206
; CURRENT APPLICATION NUMBER: US/99/424,283
; PRIOR FILING DATE: 1999-11-19
; PTO/AFFICATION NUMBER: PCI/US98/10465
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: US 60/047,568
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1924
; TYPE: DNA
; ORGANISM: Glycine max
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FEATURE:  
NAME/KEY: CDS  
LOCATION: (119)...(1588)  
US-09-424-283-5

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCAGCGGCTGGCGCCCTCTAGACTAGTGTGATCCCGGCTGCAGG 60  
DB 1881 AGCTGAGCTCCAGCGGCTGGCGCCCTCTAGACTAGTGTGATCCCGGCTGCAGG 1822

QY 61 AATTCG 66  
DB 1821 AATTCG 1816

RESULT 30  
US-09-215-221-9/c  
Sequence 9, Application US/09215221  
Patent No. 6265562  
GENERAL INFORMATION:  
APPLICANT: EILERS, MARTIN  
APPLICANT: EBERG, ANDREA  
APPLICANT: SEDLACEK, HANS-HAROLD  
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
FILE REFERENCE: 026083/0192  
CURRENT APPLICATION NUMBER: US/09/215,221  
CURRENT FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: 197 56 975.7  
PRIOR FILING DATE: 1997-12-20  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 1958  
TYPE: DNA  
ORGANISM: Murine sp.  
US-09-215-221-9

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCAGCGGCTGGCGCCCTCTAGACTAGTGTGATCCCGGCTGCAGG 60  
DB 1949 AGCTGAGCTCCAGCGGCTGGCGCCCTCTAGACTAGTGTGATCCCGGCTGCAGG 1890

QY 61 AATTCG 66  
DB 1889 AATTCG 1884

RESULT 31  
US-08-446-935-6/c  
Sequence 6, Application US/08446935  
Patent No. 6187991  
GENERAL INFORMATION:  
APPLICANT: Soeller, Walter C.  
APPLICANT: Carly, Maynard D.  
APPLICANT: Kreutler, David K.  
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II  
TITLE OF INVENTION: DIABETES MELLITUS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc.  
STREET: 235 East 42nd Street, 20th Floor  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-5755  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,935  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sheyfa, Robert F.  
REGISTRATION NUMBER: 31,304  
REFERENCE/DOCKET NUMBER: PC8153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)573-1189  
TELEFAX: (212)573-1939  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2961 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-446-935-6

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCAGCGGCTGGCGCCCTCTAGACTAGTGTGATCCCGGCTGCAGG 60  
DB 765 AGCTGAGCTCCAGCGGCTGGCGCCCTCTAGACTAGTGTGATCCCGGCTGCAGG 706

QY 61 AATTCG 66  
DB 705 AATTCG 700

RESULT 32  
US-08-646-538-6/c  
Sequence 6, Application US/08646538  
Patent No. 6027881  
GENERAL INFORMATION:  
APPLICANT: Pavlakis, George N.  
APPLICANT: Galtanakis, George A.  
APPLICANT: Stauber, Roland H.  
APPLICANT: Vournakis, John N.  
TITLE OF INVENTION: Mutant Aggrecan victoria Fluorescent  
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,538  
FILING DATE: No. 6027881 yet assigned  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 015280-249000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3699 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..3699
; OTHER INFORMATION: /note= "pbsgfp"
US-08-646-538-6

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Query Match          3.7%; Score 66; DB 3; Length 3699;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
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Db 1500 AGCTGGAGCTCCACCGGGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 1441

QY 61 AATTCG 66
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Db 1440 AATTCG 1435

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```

RESULT 33
US-09-503-222-6/c
; Sequence 6, Application US/09503222
; Patent No. 6265548
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aquorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,222
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,538
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3699 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -

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; LOCATION: 1..3699
; OTHER INFORMATION: /note= "pbsgfp"
US-09-503-222-6

Query Match          3.7%; Score 66; DB 4; Length 3699;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGAGCTCCACCGGGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 60
      |||||||
Db 1500 AGCTGGAGCTCCACCGGGGCGGCGCTCTAGAACTAGTGGATCCCGCGGCTGCAGG 1441

QY 61 AATTCG 66
      |||||
Db 1440 AATTCG 1435

RESULT 34
US-08-992-334-1/c
; Sequence 1, Application US/08992334
; Patent No. 5919678
; GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; APPLICANT: Maguin, Emmanuelle
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christie Parker & Hale, LLP
; STREET: 350 West Colorado Boulevard, Suite 500
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,334
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,752
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00248
; FILING DATE: 12-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 992/03034
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Prout, D. Bruce
; REGISTRATION NUMBER: 20958
; REFERENCE/DOCKET NUMBER: C93:31779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 795-9900
; TELEFAX: (626) 577-8800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3792 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; IMMEDIATE SOURCE:
; CLONE: pg+host4
US-08-992-334-1

Query Match          3.7%; Score 66; DB 2; Length 3792;

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Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGCTGAGACTAGTATCCCGGCTGAGG 60  
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Db 3580 AGCTGAGCTCCACCGCGGCTGAGACTAGTATCCCGGCTGAGG 60

QY 61 AATTCG 66  
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Db 3520 AATTCG 3515

RESULT 35  
US-08-302-752-1/c  
Sequence 1, Application US/08302752  
Patent No. 6025190  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: THERMOSENSIBLE PLASMID  
NUMBER OF SEQUENCES: 3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/302,752  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9203034  
FILING DATE: 13-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO FR/93/00248  
FILING DATE: 12-MAR-1993  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3792 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-302-752-1

Query Match 3.7%; Score 66; DB 3; Length 3792;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGCTGAGACTAGTATCCCGGCTGAGG 60  
|||||  
Db 3580 AGCTGAGCTCCACCGCGGCTGAGACTAGTATCCCGGCTGAGG 60

QY 61 AATTCG 66  
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Db 3520 AATTCG 3515

RESULT 36  
US-08-992-334-2/c  
Sequence 2, Application US/08992334  
Patent No. 5919678  
GENERAL INFORMATION:  
APPLICANT: Gruss, Alexandra  
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE  
TITLE OF INVENTION: PLASMID  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Christie Parker & Hale, LLP  
STREET: 350 West Colorado Boulevard, Suite 500  
CITY: Pasadena  
STATE: California  
COUNTRY: United States

ZIP: 91105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/992,334  
FILING DATE: 17-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/302,752  
FILING DATE: 24-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR93/00248  
FILING DATE: 12-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92/03034  
FILING DATE: 13-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Prout, D. Bruce  
REGISTRATION NUMBER: 20958  
REFERENCE/DOCKET NUMBER: C93:31779  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 795-9900  
TELEFAX: (626) 577-8800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-992-334-2

Query Match 3.7%; Score 66; DB 2; Length 5234;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGCTGAGACTAGTATCCCGGCTGAGG 60  
|||||  
Db 5022 AGCTGAGCTCCACCGCGGCTGAGACTAGTATCCCGGCTGAGG 4963

QY 61 AATTCG 66  
|||||  
Db 4962 AATTCG 4957

RESULT 37  
US-08-302-752-2/c  
Sequence 2, Application US/08302752  
Patent No. 6025190  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: THERMOSENSIBLE PLASMID  
NUMBER OF SEQUENCES: 3  
COMPUTER READABLE FORM:-  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/302,752  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9203034  
FILING DATE: 13-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO FR/93/00248  
FILING DATE: 12-MAR-1993  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 5234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-302-752-2

Query Match  
Best Local Similarity 3.7%; Score 66; DB 3; Length 5234;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
|||||  
Db 5022 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
QY 61 AATTCG 66  
|||||  
Db 4962 AATTCG 4957

RESULT 38  
US-08-675-566-18/c  
Sequence 18, Application US/08675566  
Patent No. 6090393  
GENERAL INFORMATION:  
APPLICANT: Fischer, Laurent  
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
METHODS FOR MAKING, AND USES THEREOF  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,566  
FILING DATE: 03-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2890  
TELEPHONE: (212)840-3333  
TELEFAX: (212)840-0712  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6045 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-675-566-18

Query Match  
Best Local Similarity 3.7%; Score 66; DB 3; Length 6045;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
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Db 3159 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
QY 61 AATTCG 66  
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Db 3099 AATTCG 3094

Query Match  
Best Local Similarity 3.7%; Score 66; DB 3; Length 6045;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
|||||  
Db 3159 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
QY 61 AATTCG 66  
|||||  
Db 3099 AATTCG 3094

## RESULT 39

US-08-675-566-17/c  
Sequence 17, Application US/08675566  
Patent No. 6090393  
GENERAL INFORMATION:  
APPLICANT: Fischer, Laurent  
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
METHODS FOR MAKING, AND USES THEREOF  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,566  
FILING DATE: 03-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2890  
TELEPHONE: (212)840-3333  
TELEFAX: (212)840-0712  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-675-566-17

Query Match  
Best Local Similarity 3.7%; Score 66; DB 3; Length 6244;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
|||||  
Db 3358 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
QY 61 AATTCG 66  
|||||  
Db 3298 AATTCG 3293

Query Match  
Best Local Similarity 3.7%; Score 66; DB 3; Length 6244;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
|||||  
Db 3358 AGCTGGAGCTCCACGGGCTGGGCGCGCTCTAGAACTAGTGGATCCCGGGCTGAGG 60  
QY 61 AATTCG 66  
|||||  
Db 3298 AATTCG 3293

## RESULT 40

US-08-675-566-16/c  
Sequence 16, Application US/08675566  
Patent No. 6090393  
GENERAL INFORMATION:  
APPLICANT: Fischer, Laurent  
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
METHODS FOR MAKING, AND USES THEREOF  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,566  
FILING DATE: 03-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2890  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)840-3333  
TELEFAX: (212)840-0712  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6447 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-675-566-16

Query Match 3.7%; Score 66; DB 3; Length 6447;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTAGAACTAGTGGATCCCGGCGTGCAGG 60  
DB 3561 AGCTGAGCTCCACCGCGGTGGCGCGCTAGAACTAGTGGATCCCGGCGTGCAGG 3502

QY 61 AATTCG 66  
DB 3501 AATTCG 3496

RESULT 41  
US-08-675-566-4/c  
Sequence 4, Application US/08675566  
Patent No. 6090393  
GENERAL INFORMATION:  
APPLICANT: Fischer, Laurent  
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,566  
FILING DATE: 03-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2890  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)840-3333  
TELEFAX: (212)840-0712  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6578 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-675-566-4  
Query Match 3.7%; Score 66; DB 3; Length 6578;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTAGAACTAGTGGATCCCGGCGTGCAGG 60  
DB 4516 AGCTGAGCTCCACCGCGGTGGCGCGCTAGAACTAGTGGATCCCGGCGTGCAGG 4457

QY 61 AATTCG 66  
DB 4456 AATTCG 4451

RESULT 42  
US-08-675-566-15/c  
Sequence 15, Application US/08675566  
Patent No. 6090393  
GENERAL INFORMATION:  
APPLICANT: Fischer, Laurent  
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,566  
FILING DATE: 03-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2890  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)840-3333  
TELEFAX: (212)840-0712  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6612 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-675-566-15

Query Match 3.7%; Score 66; DB 3; Length 6612;  
Best Local Similarity 100.0%; Pred. No. 1.7e-23;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGAGCTCCACCGCGGTGGCGCGCTAGAACTAGTGGATCCCGGCGTGCAGG 60  
DB 3726 AGCTGAGCTCCACCGCGGTGGCGCGCTAGAACTAGTGGATCCCGGCGTGCAGG 3667

QY 61 AATTCG 66  
DB 3666 AATTCG 3661

RESULT 43  
US-08-992-334-3/c

MOLECULE TYPE: DNA (genomic)

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RESULT 44
US-08-302-752-3/c
; Sequence 3, Application US/08302752
; Patent No. 6025190
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```





? FILING DATE: 13-MAR-1997  
 ? CLASSIFICATION: 424  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: MAKI, David J.  
 ? REGISTRATION NUMBER: 31,392  
 ? REFERENCE/DOCKET NUMBER: 210121.417C6  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (206) 622-4900  
 ? TELEFAX: (206) 682-6031  
 ? INFORMATION FOR SEQ ID NO: 14:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 1058 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? US-08-818-111-14

Query Match 3.7%; Score 65; DB 4; Length 1058;  
 Best Local Similarity 100.0%; Pred. NO. 5.3e-23;  
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTCGACGCGGCTGCGCGCTGTAGAACTAGTGGATGCGCGCGCGCTGCGCGAAATTGCGC 68  
 |||  
 DB 1 CTCGACGCGCGCTGCGCGCTGTAGAACTAGTGGATGCGCGCGCGCTGCGCGAAATTGCGC 60

QY 69 ACGAG 73  
 ||||  
 DB 61 ACGAG 65

Search completed: October 31, 2002, 11:46:25  
 Job time : 154 secs